#### STIC-Biotech/ChemLib

From:

Ibrahim, Medina A.

Sent: To:

Tuesday, May 27, 2003 7:21 AM STIC-Biotech/ChemLib

Subject:

09/977, 137

(STIC)

Please search the following:

- 1. SEQ ID NO:3-4.
- 2. oligo search of SEQ ID NO:3-4.

Please search both commercial and patent databases (including pending). Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9E03 mailbox-9E12 (703)306-5822

Searcher:\_\_\_\_\_ Phone:\_\_\_\_\_ Location:\_\_\_\_ Date Picked Up: 5 PK
Date Completed: 4 Searcher Prep/Review: Clerical:\_ Online time:\_\_\_\_\_

TYPE OF SEARCH: NA Sequences:\_\_\_\_\_ AA Sequences:\_\_\_\_\_ Structures:\_\_\_\_\_ Bibliographic:\_\_\_\_\_ Litigation:\_\_\_\_\_ Full text: Patent Family:\_\_\_\_\_ Other:\_\_\_\_\_

VENDOR/COST (where applic.) STN:\_\_\_\_\_ DIALOG:\_\_\_\_\_ Questel/Orbit:\_\_\_\_\_ DRLink:\_\_\_\_\_ Lexis/Nexis:\_\_\_\_\_ Sequence Sys.:\_\_\_\_\_\_\_
WWW/Internet:\_\_\_\_\_ Other (specify):\_\_\_\_\_

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Maximum DB seq·length: 2000000000
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#### RESULT 1 C91774/c DEFINITION FEATURES REFERENCE KEYWORDS ACCESSION AUTHORS ORGANISM JOURNAL C91774 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-group) cDNA clone E31517\_1A, mRNA sequence. Oryza sativa (japonica cultivar-group). Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhattoideae; Oryzeae; Oryza. 1 (bases 1 to 305) Sasaki,T. and Yamamoto,K. Rice cDNA from panicle Unpublished (1997) Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, Tel: 81-298-38-7441 Fax: 81-298-38-7468 C91774.1 GI:3061142 PROJECT ='RGP' 305-8602, tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/ Location/Qualifiers Japan Tsukuba, EST 04-APR-2002

COMMENT

TITLE

SOURCE

VERSION

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Result

No.

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Match Length DB

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Description

SUMMARIES

Query

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C91774 C91774 Rice B1480603 EST0056 H BE791590 601585915 A1824830 wb02d07.x BE227306 894030B09 AW628641 hi37h06.x

source

/organism="Oryza sativa (japonica cultivar-group)"

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                   DEFINITION
                                                   BE791590
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     1099 bp mRNA linear EST 20-
601585915F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940395
mRNA sequence
                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: O'Connell, MA
Department of Agronomy and Horticulture
New Mexico State University
MSC 30, P.O. Box 30003, Las Cruces, NM 88003, USA
Tel: 505 646 5172
Fax: 505 646 6041
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Nevarez,J.G. and O'Connell,M.A.
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: moconnel@nmsu.edu
Insert Length: 1200 Std
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Similarity 100.08;
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/cultivar="Early Scotch Bonnet"
/db_xref="taxon:80379"
/clone="Jn 51"
                                                                                                                                                                                                                                                                         /note="Organ: leaf; Vector: Uni-zap xR; Site_1: EcoR1; Site_2: Xho 1"
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/dev_stage="drought-stressed"
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110 c 92 g
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/db_xref="taxon:39947"
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  Tumor Gene Index Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                             A1824830 344 bp mRNA linear EST 16-DEC-1999 wb02d07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304493 3' similar to SW:HMG2_CHICK P26584 HIGH MOBILITY.GROUP PROTEIN HMG2;;
                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 344)
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                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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Tissue Procurement: DCTD/DTp
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM790 row: m column: 04
High quality sequence start: 7
High quality sequence start: 7
LCCATION/Qualifiers
1 1000
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National Institutes of Health, Mammalian Gene Collection (MGC)
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[ (bases 1 to 1099)
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Emmert-Buck, M.D., Ph.D.
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 321 c 342 g 215 t
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/db_xref="taxon:9606"
/cione="IMAGE:3940395"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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100.0%; Pred. No.
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CDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Clone distribution information can be
Clone distribution can be clone distribution can be
Clone distribution can be clone distribution can be clone distribution can be clone distribution can be close distribution can be clo
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Seq primer: -40UP from Gibco
High quality sequence stop: 264.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   894030809.x3 C. reinhardtii CC-1690, normalized, Lambda Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
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                                                                                                                                                                                                                                                                                                                                                                      Tel: 919 613 8164
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Elizabeth H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durham, NC 27708-1000, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                          Email: chlamy@duke.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 362)
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/clone_lib="NCI_CGAP_GC6"
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/db_xref="taxon:9606"
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/lab_host="DH108"
                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2974523"
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SOURCE

KEYWORDS VERSION

COMMENT

Query Match Best Local Similarity

Matches

18;

Conservative

100.0%;

5.6%; Score 18; DB 10; 100.0%; Pred. No. 1.5e+0; ive 0; Mismatches

1.5e+02;

Length 398;

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GGGAATGTTTCCTGCCCG 147

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                                                                                                                                                                                                                                          179 CCCACTGCGAGGAGGCCA 196
BM487398
425 bp mRNA linear EST 07-FEB-200: pgm2n.pk004.hl Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk004.hl 5' similar to gb|AAK15544.1 (AF346565) signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@lidwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-GN0070-120
900-022-E10&t3=2000-09-12&t4=1)
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                               /note="organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/clone_lib="GN0070"
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Pred. No.
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library, USDA/IFAFS Animal Genome Project Unpublished (2002)
                      1 (bases 1 to 425)
Porter, T.E. and Cogburn, L.A.
ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
                                                                                                                                                                                                                                                                                   BM491850
425 bp mRNA linear EST 07-FEB-2002
pgp2n.pk007.j9 Normalized Chicken Pituitary/Hypothalamus/Pineal
Library (pgp2n) Gallus gallus cDNA clone pgp2n.pk007.j9 5' similar
to gb|AAK15544.1 (AF346565) signal sequence receptor beta subunit
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                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                       Gallus gallus
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                                                                                                                                                                                                                                                               [Xenopus laevis], mRNA sequence.
BM491850
                                                                                                                                                                                                   cnicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cogburn@udel.edu,
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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BM487398
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/lab_host="E. coli EMDH10B"
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growth plate"
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/clone=lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
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Strains 90 & 21"
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COMMENT

Contact: Larry A. Cogburn University of Delaware

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Location/Qualifiers
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Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
                                                                                                                                                                                                                                   Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-3345
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                           Burnside, J., Morgan, R.W. and Cogburn, L.A. Chicken ESTs from a normalized liver library
                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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  83 a
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/db_xref="taxon:9031"
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/tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
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/clone_lib="Normalized Chicken
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                                                                                                 /db_xref="taxon:9031"
/clone="pglln.pk001.d18"
/clone_lib="Normalized Liver Library"
/note="Vector: pCMVSPORT 6"
122 c 134 g 113 t
                                       /tissue_type="liver"
/lab_host="E.coli EMDH10B"
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                                                                          /sex="Male and Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins C., M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsona, J., Prance, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 527 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
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                                    Conservative
                                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same form as the ferry very superference of the same constructed from the same form.
                                                                                                                                                                                                                                                                                                                                        same fetus as the fetal lung library, Soares fetal lung NbHL19M."
75 c 98 g 132 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:1281180"
/db_xref="taxon:9606"
/clone="IMAGE:364476"
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                               Cogburn, L.A. and Monsonego-Ornan, E.
                                                                                                                                                        Gallus gallus
                                                                                                                                                                                                                                                        pgm2n.pk002.cl Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk002.cl 5′ similar to gb|AAK15544.1 (AF346565) signal sequence receptor beta subunit [Xenopus laevis], mRNA sequence.
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                                                                           Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717,
Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 467)
Burnside, J., Morgan, R.W. and Cogburn, L.A.
Chicken ESTS from a normalized liver library
Unpublished (2001)
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TRANSLOCON-ASSOCIATED PROTEIN, BETA SUBUNIT PRECURSOR (TRAP-BETA)
(SIGNAL SEQUENCE RECEPTOR BETA SUBUNIT) (SSR-BETA) (GP25H)
(SIGNAL SEQUENCE RECEPTOR BETA SUBUNITY (SSR-BETA) (GP25H)
(SSR-BETA) (GP25H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: joan@UDel.Edu, www.chickest.udel.edu
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  from Normalized Chicken Breast Muscle,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pcMVSPORT_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
/db_xref="taxon:9031"
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/sex="Male and Female"
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    Email: asimpson@ludwig.org.br
This sequence was derived from the
Project. This entry can be seen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                     Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 GGAGGCCAGCAGCCTGGC 32
                                                                        Fax: +55-11-2707001
                                                                                         Tel: +55-11-2704922
                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                         Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                               Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                         sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF850925 495 bp mRNA linear MR4-EN0075-241100-001-f07 EN0075 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                 Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Townsend Hall, Newark, DE 19717,
Tel: 302-831-1335
Fax: 302-831-2822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cogburn@udel.edu, www.chickest.udel.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Larry A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="pgm2n.pk002.c1"
/clone_lib="Normalized Chicken Breast Muscle, Le
and Epiphyseal Growth Plate cDNA library (pgm2n)
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
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,11 weeks):growth plate(1d,7d,14d post-hatch)"
//lab_host="E. coli EMDH10B"
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FAPESP/LICR Human the following URL
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MEDLINE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through Research Genetics Thum. (info@image.linl.gov). INAGE ID- 1774925
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF550791 512 bp mRNA linear EST 12-DI UI-R-CO-jp-e-05-0-UI.rl UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-jp-e-05-0-UI 5', mRNA sequence.
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Normalization and subtraction: two approaches to facilitate gene
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241100-001-f07&t3=2000-11-24&t4=1)
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/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-A1
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-jp-e-05-0-UI"
                                                                                                                                               /clone_lib="UI-R-CO"
                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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Sciurognathi; Muridae; Murinae;
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ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                            and UI-R-El libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-Al and UI-R-El library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described
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2003, 09:04:39
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hes 0;
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Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/
2: /cgn2_6/ptodata/1/
3: /cgn2_6/ptodata/1/
4: /cgn2_6/ptodata/1/
5: /cgn2_6/ptodata/1/
6: /cgn2_6/ptodata/1/
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(without alignments)
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                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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4411529
4 US-09-103-840A-2
4 US-09-103-840A-1
US-08-675-508-10
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US-08-675-508-11
US-08-675-508-11
US-08-675-508-11
US-08-675-508-11
US-08-465-380-115
US-08-486-399-115
US-08-486-399-115
US-08-486-399-115
US-08-486-391-115
US-08-486-391-115
US-08-486-391-115
US-08-486-391-115
US-09-249-471-115
US-09-249-481-115
US-09-249-481-115
US-08-465-380-113
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  Sequence 2, Appli Sequence 13, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 115, Appli Sequence 111, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 28, Appli Sequence 29, Appli Seque
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STRAIN 840A	ed. No. 4 Mismatches		STRAIN	ENTS	0-478-29 6-397-112 6-397-113 6-399-114 6-399-114 6-399-114 1-955-112 1-965-113 1-965-114 6-110A-27 6-110A-28 4-641-112 4-641-113 4-641-113 4-641-113
ANALYSIS IN	4; 0; Inde	itions	ANALYSIS IN		
N MYCOBACTERIUM	1s	hout t	MYCOBACTERIUM		Sequence
ERIUM	Gaps 0	sequence	SR10M		29, Appl 1112, App 1114, App 1112, App 1113, App 1114, App 1115, App 116, App 117, App 117, App 117, App 117, App 118, App 119, App 119, App 119, App 1119, App

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RESULT 4
US-08-675-508-10/c
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            Sequence 10, Application US/08675508 Patent No. 5856136
                                                                                                                                                                  Matches
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GENERAL INFORMATION:
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                             / Match 5.0%; Sc Local Similarity 100.0%; F Conservative 0;
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100.0%; Pred. No. 4.4;
ative 0; Mismatches
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                                                                                                                                                                             Score 16; DB 2; Length 261; Pred. No. 21;
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                                                                                                                                                                 Mismatches
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         OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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LIBRARY: BRSTT
CLONE: 604702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: Filed Herew ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,
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TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
REFERENCE/DOCKET NUMBER: PF-0066 US
                                                                                                                                    COMPUTER:
                                                                                                                                                                                                               STATE:
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Local Similarity 100.0%; Pred. No. 21;
nes 16; Conservative 0; Mismatches
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CITY: Palo Alto
STATE: CA
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AU-Young, Janice
NOVEL HUMAN STEM CELL ANTIGENS
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                                                                                                                               IBM Compatible
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SYSTEM: DOS
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RESULT 6
US-08-675-508-9/c
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                                                            Matches
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INFORMATION FOR SEQ ID NO:
                                                                                       Query Match
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                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675
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CITY: Palo Alto
CMATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                             FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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Local Similarity 100.0%; Pred. No. 21;
nes 16; Conservative 0; Mismatches
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CLONE: 728784
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                                                                       Local Similarity
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27 CCAGCAGCCTGGCCGA 12
                              20 CCAGCAGCCTGGCCGA 35
                                                          16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             us/08/675,508

 Mismatches

                                                                          Score 16; pred. No.
                                                                                                                                                                                                                                                                                                                                     PF-0066 US
                                                                                          DB 2;
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                                                                                          Length 278;
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; Sequence 11, Application US/08675508 ; Patent No. 5856136
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US-08-675-508-11/c
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                                                                                                                                                                                                                                                                                               RESULT 8
US-08-675-508-12/c
                                                                                                                                                                                                                                                            Sequence 12, Application US/08675508 Patent No. 5856136
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APPLICANT: Au-You
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                              TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMEDIA...
LIBRARY: BAUL
TONE: 606246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 31/4 FOR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                         STREET: 3174 FOR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%; es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                               STATE:
                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                COUNTRY: UZIP: 94304
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                               27 CCAGCAGCCTGGCCGA 12
                                                                                                                                                                                                                                                                                                                                                                                              20 CCAGCAGCCTGGCCGA 35
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3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415-845-4166
                                                                                                                                                                                                             Au-Young, Janice
VENTION: NOVEL HUMAN STEM CELL ANTIGENS
                                                                                               U.S.
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FastSEQ Version 1.5
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                                                  Diskette
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US-08-746-397-1/c
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                                                                              TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                           NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/7
FILING DATE: 11/8/96
CLASSIFICATION: 424
                                                                                                                                                                                            FILING DATE: 11/9/95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NI ET AL.
TITLE OF INVENTION: Human Stem Cell Antigen 2
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: BRSTN
CLONE: 637479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Filed Herew.
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                         STRANDEDNESS:
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APPLICATION NUMBER: US
                                                         LENGTH:
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REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                         NUCLEIC ACID
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                                                       1163 BASE PAIRS
              LINEAR
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100.0%; Pred. No.
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21;
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                                                           Matches
                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 115,
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                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NEMATOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                          Local Similarity
les 15; Conserv
                                                                                                                                                                                                                       TELEFAX: (213)
TELEX: 67-3510
                                                                                                                                                                                                                                                                                          NAME: BIGGS, SUZANNI
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5" Di
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 30
                           63 GATGGCCGACTTGGC 77
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GATGGCCGACTTGGC 44
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5863894
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                                                                                                                                                                          45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peter W. Bergum
                                                        Conservative
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                                                                                                                                                                                                                                                  (213) 489-1600
                                                                                                                                             single
                                                                                                                                                                                                                                     955-0440
                                                    4.7%; Score 15; DB 2;
100.0%; Pred. No. 74;
tive 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatc
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; Sequence 30, Application US/08480478

US-08-480-478-30

RESULT 11

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                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                              Sequence 115, Application US/08486397 Patent No. 5866542
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                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Surc
CITY: Los Angeles
STATE: California
or S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NEMATODE-EXTRACTED ANTITITLE OF INVENTION: COAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/326,1
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                              APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                               63 GATGGCCGACTTGGC 77
                                                                                                                                                                                                                                                                                                              30 GATGGCCGACTTGGC 44
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUGO STANSSENS; JORIS HILDA LIEVEN MESSENS; MARC JOZEF LAUMEREYS; YVES RENE LAROCHE; LAURENT STEPHANE JESPERS; and YANNICK GEORGES JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEORGE P. VLASUK; PATRICK ERIC
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357
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US-08-486-397-115
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US-08-486-399-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATENL MY. PATENLE PATENLE MY PAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. SOPTWARE: WORD PERfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/326,111
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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CORRESPONDENCE ADDRESS:
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                                SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
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APPLICATION NUMBER:
                                                                                                OPERATING SYSTEM:
                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                       IBM P.C. DOS 5.0
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       US/08/486,399
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEZX: 67-3510
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO: 115:
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                                                                                                                                                                            APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
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ZIP: 90071
COMPUTER READABLE FORM:
COMPUTER
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TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
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FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
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                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CON OPERATING SYSTEM:
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STATE: California
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STREET: 633 West F:
STREET: Suite 4700
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                                               67-3510
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                                                                              (213) 955-0440
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633 West Fifth Street
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DN: 530
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                              Matches
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                                                         Query Match
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                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Vers. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 633 West F11
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                              Local Similarity
mes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1bm ... IBM F... OPERATING SYSTEM: IBM F... OPERATING SYSTEM: TON 1.5
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                                                                                                  STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/326,110A FILING DATE: 18 OCTOBER 1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                             LENGTH:
                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%; Pred. No. 74 les 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
63 GATGGCCGACTTGGC 77
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                                                                                                                           nucleic acid
                                                                                                                                            45 base pairs
                            Conservative
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633 West Fifth Street
                                                                                                                                                                                                     (213) 955-0440
                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUGO STANSSENS; JORIS HILDA
LIEVEN MESSENS; MARC JOZEF
LAUWEREYS; YVES RENE LAROCHE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAURENT STEPHANE JESPERS; and YANNICK GEORGES JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEORGE P. VLASUK; PATRICK ERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                   SUZANNE L.
SUZANNE L.
20,158
                                                                                                                single
                                       4.7%; Score 15; DB 2; 100.0%; Pred. No. 74;
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COAGULANT PROTEIN
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Pred. No.
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                        Indels
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Search completed: June 2, 2003, 09:05:42 Job time : 52 secs

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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321
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2: //cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: //cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: //cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: //cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
6: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
9: //cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
9: //cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: //cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
11: //cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: //cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13: //cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: //cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: //cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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  2, 2003, 08:35:40; Search time 136 Seconds (without alignments) 3182.538 Million cell updates/sec
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                                       US-09-712-363-25
US-09-796-692-5769
US-10-040-862-5723
US-09-796-692-5723
US-09-796-692-3737
US-09-796-692-3737
US-09-796-692-5607
US-10-040-862-5607
US-10-040-862-5607
US-10-040-862-5607
US-10-040-862-5607
US-10-040-862-5680
US-10-040-862-6280
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US-09-918-995-20836
                  US-09-934-586A-13
US-09-934-586A-10
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                                           Sequence 5769, Ap
Sequence 5769, Ap
Sequence 5723, Ap
Sequence 5723, Ap
Sequence 5667, Ap
Sequence 5667, Ap
Sequence 5667, Ap
Sequence 5667, Ap
Sequence 5260, Ap
Sequence 6280, Ap
Sequence 6280, Ap
Sequence 55, Appl
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sequence 20836, A
sequence 25, Appl
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US-09-960-352-10733	US-09-783-590-6603	US-09-864-761-748	US-09-783-590-2269	US-09-833-301 1000	10 00 000 000 100 000 000 000 000 000 0	116-00-023-876-4927	rrs-09-925-299-474	US-09-925-299-474	US-09-923-876-2556	08-09-923-070-3471	12 00 000 000 1 12 00 000 000 1	WC-00-738-626-1	TIS-09-900-449A-3	US-09-764-847-1596	US-10-092-154-1590	- 10 000 1F1 1606	76 10-009-841-105	115-09-804-073-1	ns-09-738-626-1656	US-10-101-747-1	05-09-8T6-80-SD	OS-03-310 OOF 13450	75-00-018-995-17595	ne-09-960-352-2232	ns-09-983-965-3887	US-09-867-550-653	US-09-934-586A-12	US-09-934-586A-11	10 00 004 E063-11	116-09-934-586A-9
sequence rovos	Sequence boos, AP	(00)	740,	2269.	Sequence 1856, Ap	Sequence 4927, AP	Sequence 4/4, APP	* *	•	COTION 0556 AD	sequence 3471, Ap	Sequence 1, Appli	Sequence 3, APPLI	Sequence 1999's	comence 1596. Ap	1596	Sequence 105, App	Sequence 1, Appl1	Sequence Lobo, AP	Seducinco Ti	,	Segmence 13450, A	Sequence 17595, A	•		2 0	Gequence 53 App	12	Sequence 11, Appl	Sequence 9, Appli

# ALIGNMENTS

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LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)... (463)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-918-995-19156
Sequence 19156, Application US/09918995
Publication No. US20030073623A1
Fequence 20836, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED;
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES;
                                                                                                                                                                                                                                     밁
                                                                                                                                         US-09-918-995-20836
                                                                                                                                                                    RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT FILLING DATE: 2001-07-30
CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PRIOR TILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 19156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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17; Conserva
                                                                                                                                                                                                                                                                                                                              Conservative
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FILE REFERENCE: 20411-756

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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-25
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
                                                                                   Matches
                                                                                                                  Query Match
                                                                                                                                                                                                                                 SEQ ID NO 25
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                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09712363 Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY (
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20836
                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Eisenberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: (1)...(484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(484)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/134,093
FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/134,092
FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
876 GGCCGACTTGGCGCGCA 892
                                    66 GGCCGACTTGGCGCGCA 82
                                                                               1 Similarity
17; Conserv
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                                                                           Conservative
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                                                                                            100.0%;
                                                                                       5.3%; Score 17;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.3%; Score 17; DB 9; 100.0%; Pred. No. 7.5;
                                                                         0;
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                                                                       Mismatches
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                                                                                                    DB 9; Length 1356;
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Sequence 5769, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
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  APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Methor, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
FILE REFERENCE: 014058-013520US
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5769, Application US/09796692
PUDILication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILL REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
CURRENT APPLICATION NUMBER: US/10/040,862
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5769
LENGTH: 151
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NAME/KEY: unsure
LOCATION: (43)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/218,950 PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
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PRIOR FILING DATE: 2000-05-22
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PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
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OTHER INFORMATION: n=A,T,C or G
US-10-040-862-5769
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PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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PRIOR APPLICATION NUMBER: US 60/186,126
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
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Best Local 9
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PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/223,378 PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/796,692 PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                   APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: MANNION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION UNDER: US/09/796,692
CURRENT APPLICATION NUMBER: US/08/126
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (43)
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                                                                                         PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
                                                                       APPLICATION NUMBER: 60/200,779
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-5723
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                                                                                                                                                                                                                                                          PRIOR PLILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR PRIOR PAPELICATION NUMBER: US 60/200,779

PRIOR FILLING DATE: 2000-04-28

PRIOR FILLING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILLING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR FILLING DATE: 2000-05-04

PRIOR FILLING DATE: 2000-05-04
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
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PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5723, Application US/10040862
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PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR EILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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PRIOR APPLICATION NUMBER: US 60/223,416
                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-07-14
                                                                                                                                   PRIOR APPLICATION NUMBER:
                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                            PRIOR
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                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
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Corixa Corporation
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[00.0%; Pred. No.
                                                                                                                                              US 60/223,378
                                                                                                                                                                                                                                   US 60/222,903
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32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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LENGTH: 154

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APPLICANT: Galger, Alexander
APPLICANY: Algate, Paul A.

APPLICANY: Algate, Paul A.

APPLICANY: Algate, Paul A.

FITLE OF INVENTION: HEMATOLOGICAL MALICHARCIES

CURRENT APPLICATION HEMATOLOGICAL MALICHARCIES

CURRENT APPLICATION NUMBER: 5007-03-01

PRIOR APPLICATION NUMBER: 5007-03-01

PRIOR APPLICATION NUMBER: 60/200, 545

PRIOR APPLICATION NUMBER: 60/200, 545

PRIOR APPLICATION NUMBER: 60/200, 303

PRIOR APPLICATION NUMBER: 60/200, 309

PRIOR APPLICATION NUMBER: 60/201, 309

PRIOR APPLICATION NUMBER: 60/201, 309

PRIOR APPLICATION NUMBER: 60/203, 319

PRIO
Sequence 5607, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
                                                                                                 US-09-796-692-5607
                                                                                                                                    RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3737 LENGTH: 158
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US-09-796-692-3737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                         133 GGATCCTCAGGCACCC 148
                                                                                                                                                                                                                                                                  166 GGATCCTCAGGCACCC 181
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                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 GGATCCTCAGGCACCC 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-08-07
JOS: 9597
                                                                                                                                                                                                                                                                                                     5.0%; Score 16; DB 9; Length 158; 100.0%; Pred. No. 32; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0%; Score 16;
100.0%; Pred. No.
ative 0; Mismatc
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
FILE REFERENCE: 2077.001200
CURRENT FILING DATE: 2077.001200
CURRENT FILING DATE: 2007.03-01
PRIOR APPLICATION NUMBER: US/09/796.692
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR PELICATION NUMBER: 60/200,545
PRIOR REPLICATION NUMBER: 60/200,545
PRIOR REPLICATION NUMBER: 60/200,545
PRIOR REPLICATION NUMBER: 60/200,545
PRIOR PRILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR APPLICATION NUMBER: 60/223,416
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; ORGANISM: Homo sapiens
US-09-796-692-5607
                       PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
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PRIOR APPLICATION NUMBER: 60/200,999
                                                                                                                                                                                                                                                                                                                               APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
FILE REFERENCE: 2077.001200
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SEQ ID NO 5607
LENGTH: 158
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Best Local
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PRIOR FILING DATE: 2000-08-04
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100.0%; Pred. No. 32;
ative 0; Mismatches
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-796-692-5667
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PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
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US-10-040-862-3737
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
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PRIOR APPLICATION NU
PRIOR FILING DATE: 2
PRIOR APPLICATION NU
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
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                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/223,416
                                       PRIOR APPLICATION NUMBER: US 09/796,692 PRIOR FILING DATE: 2001-03-01
                                                                                    PRIOR FILING DATE:
                                                                                       PRIOR APPLICATION NUMBER: US 60/223,378 PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-03
                   NUMBER OF
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                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/206,201
                                                                                                                                                                                                                                                                               FILING DATE:
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SEQ ID NOS: 10467
FastSEQ for Windows Version 3.0
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Corixa Corporation
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                                                                                                                                           2000-08-04
                                                                                                                                                                                                                                                                                    2000-05-22
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100.0%; Pred. No.
                           10467
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-040-862-3737
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US-10-040-862-5607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                              SEQ ID NO 5607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
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CURRENT FILING DATE: 2001-11-06
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
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PRIOR FILING DATE: 2000-04-28
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                                                                        Matches
                                                                                                             Query Match
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/223,416 PRIOR FILING DATE: 2000-08-04
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PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,950 PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                      ENGTH: 158
                                                                                           Local
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                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/223,378 FILING DATE: 2000-08-07
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                                    166 GGATCCTCAGGCACCC 181
133 GGATCCTCAGGCACCC 148
                                                                                             Similarity
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Corixa Corporation
                                                                        Conservative
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100.0%; Pred. No.
                                                                          5.0%; Score 16; DB 9; Length 158; 100.0%; Pred. No. 32; tive 0; Mismatches 0; Indels
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RESULT 14
US-09-796-692-6280
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ORGANISM: Homo sapiens
US-10-040-862-5667
                                                                                                                                                                                                                                      Sequence 6280, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Agrate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/200,545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 014058-0135200S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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APPLICATION NUMBER: US 60/223,378
FILING DATE: 2000-08-07
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Corixa Corporation
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100.0%; Pred. No.
tive 0; Mismatc
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SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6280

LENGTH: 159

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1)
OTHER INFORMATION: n-A,T,C or G
US-09-796-692-6280
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6280, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corporation
TITTLE CORIXA CORPORATION
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                                                                                              PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PILING DATE: 2000-04-28
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/040,862 CURRENT FILING DATE: 2001-11-06 PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: US 60/190,479 PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
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Best Local 9
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NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 2000-08-07
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PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
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                   APPLICATION NUMBER: US 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
APPLICATION NUMBER: US 60/206,201
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Corixa Corporation
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PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: US 60/218,950

PRIOR APPLICATION NUMBER: US 60/227,903

PRIOR APPLICATION NUMBER: US 60/223,416

PRIOR APPLICATION NUMBER: US 60/223,416

PRIOR APPLICATION NUMBER: US 60/223,378

PRIOR APPLICATION NUMBER: US 60/223,378

PRIOR APPLICATION NUMBER: US 60/223,378

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2001-03-01

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PRIOR APPLICATION NUMBER: US 60/223,378

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIE

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48	55	57	57	57	57	57	57	64	117	Score
41.0	47.0	48.7	48.7	48.7	48.7	48.7	48.7	54.7	100.0	Query Match
118	144	117	117	117	117	117	117	117	117	Query Match Length DB
23	23	23	23	23	23	23	23	23	23	1
AAU97554	AAU97551	AAU97559	AAU97558	AAU97557	AAU97556	AAU97555	AAU97553	AAU97560	AAU97552	ID
Synthetic cadmium/	Shigella flexneri	Synthetic cadmium/	Synthetic cadmium/	Synthetic cadmium/			Synthetic cadmium/	Synthetic cadmium/	Synthetic MerR che	Description

45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	ㄷ
6	6	6	7	7	7	7	7	7	7	7	7	7	7	7	8	œ	œ	œ	œ	80	8	8	œ	œ	œ	œ	œ	00	œ	œ	10	10	24	29
5.1	5.1	5.1	6.0		٠			•		6.0			٠						٠	٠	6.8				6. 8		6.8		•	•				4.
25	19	19	2659	1122	515	378	359	192	192	192	179	165	161	158	659	659	448	396	396	396	254	254	205	10	œ	œ	<b>&amp;</b>	8	8	<b>&amp;</b>	10	10	159	144
23	23	21	22	22	21	21	21	22	22	22	21	21	22	21	22	22	22	22	22	20	22	20	20	22	23	23	22	22	22	19	23	22	15	20
AAU88121	ABG68205	AAY91226	ABB68426	ABB61604	AAG42522	AAG42523	AAG42524	AAU21776	AAM96372	ABB10936	AAG15365	AAG15366	AAU21632	AAG15367	AAB46427	AAB46426	AAB46425	AAB46423	AAB46420	AAW93966	AAB46421	AAW93969	AAW93967	AAB99027	ABB57464	ABB77486	AAB68616	AAB35442	AAB35433	AAW59212	AAU80475	AAY97662	AAR49668	AAY01816
Insulin/insulin-li	Measles virus idea	d meas	-		Arabidopsis thalia				$\alpha$	Human ovarian and/	ţ.				Bilin binding-prot	5	ם	binding.	binding-p	id pBBP2(			21	Streptavidin detec	STREP tag II pepti		Strep-Tag II seque	Nascent protein de	Epitope peptide #3	Ž	Peptide STREP tag.	enz	Protein product of	MerR protein which

# ALIGNMENTS

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AAU97552
                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
                                                                                                                                                                                                              Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent catio
          N-PSDB; ABK52207, ABK52213
                       WPI; 2002-435437/46.
                                                                                                                                   18-APR-2002.
                                                                                                                                                                                                                                                                       Synthetic MerR chelon variant.
                                                                                                                                                                                                                                                                                               13-AUG-2002
                                                                                                                                                                                                                                                                                                                      AAU97552;
                                                                                                                                                                                                                                                                                                                                           AAU97552 standard; Protein; 117 AA.
                                           Summers AO,
                                                                                       12-OCT-2000; 2000US-240465P.
                                                                                                             12-OCT-2001; 2001WO-US31819
                                                                                                                                                          WO200230962-A2.
                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                     heavy metal binding protein; MerR.
                                                                  (UYGE-)
                                                                  UNIV GEORGIA RES FOUND INC
                                           Caguiat JJ;
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                   divalent cation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding cepton for the protein to produce a recombinant host cell and culturing classing a cid encoding the chelon protein is useful for binding cd the recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding cd divalent mercuric ions, to take up, sequester and concentrate the heavy containing the chelon protein is useful for binding containing the chelon for the invention, when capable onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated capacity expressed in enteric bacteria (which are nontoxigenic and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and conclusts of the invention are also useful in water treatment resins. CC molecules of the invention are also useful in water treatment resins. CC molecules of the invention are also useful in water treatment resins. CC invention. This sequence is one of the water chelon variant protein of the carmed chelons of the invention. Merk chelon variant protein of the carmed chelons of the invention acids 1-107 of this proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
12-OCT-2000; 2000US-240465P
                                             12-OCT-2001; 2001WO-US31819.
                                                                                          18-APR-2002
                                                                                                                                        WO200230962-A2
                                                                                                                                                                                                                                heavy metal binding protein.
                                                                                                                                                                                                                                                     enteric bacteria; toxic metal ion; mercury;
                                                                                                                                                                                                                                                                        Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein;
                                                                                                                                                                                                                                                                                                                                                                        Synthetic cadmium/mercury ion binding chelon protein #8
                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU97560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU97560 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 117; DB 23; Pred. No. 3.1e-115;
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                                                                                                                                                                                                                                                   divalent cation;
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AAU97553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which binds mercuric ions. The invention is useful for recombinantly colors are producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding cd divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when claims from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and celimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino caid sequence represents one of a collection (AAU97553-AAU97560) of synthetic cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                        irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalen
                                                                                                                                                                                Synthetic cadmium/mercury ion binding chelon protein #1.
                                                                                                                                                                                                                                                                                                                AAU97553 standard; Protein; 117 AA
                                                         heavy metal binding protein.
                                                                                                                                            Mercuric ion;
                                                                                                                                                                                                                             13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-435437/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYGE-) UNIV GEORGIA RES
                                                                                                                                                                                                                                                                                                                                                                                                                    114 QFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 QFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                           (first entry)
                                                                                                                                        contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.7%; Score 64; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 117;
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                                                                              divalent cation
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cell capable of expressing a chelon coding sequence with a vector cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing the recombinant host cell inder conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding cell ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when cell inmobilised onto a solid support, is useful for concentrate the heavy introduced in the invention and cell inmobilised onto a solid support, is useful for concentrating heavy metal cell inmobilised onto a solid support, is useful for concentrating heavy metal cell inmobilised onto a solid support, is useful for concentrating heavy metal cell inmobilised onto a solid support, is useful for concentrating heavy metal cell inmobilised onto a solid support, waste streams or contaminated cell inmobilised onto a solid support, waste streams or contaminated cell inmobilised onto a solid support, waste streams or contaminated cell instance of a cell provided in the invite streams or contaminated cell instance of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cell instance represents one of a collection (AAU9753-AAU9756) of acid sequence represents one of a collection (AAU9753-AAU9756) of the invention.

CC of this sequence is one of the heavy metal binding proteins termed chelons cell in the invention of the heavy metal binding proteins termed chelons.
                                                                                                                                                                                                                                                                                                                                                                                         В
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000; 2000US-240465P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001; 2001WO-US31819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summers AO, Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                               Synthetic cadmium/mercury ion binding chelon protein #3.
                                                                                                                                                                                    13-AUG-2002 (first entry)
                                                                                                                                                                                                                             AAU97555:
                                                                                                                                                                                                                                                                          AAU97555 standard; Protein; 117 AA
                                                                                 Mercuric ion; contaminated soil; ground water; hydroponic solution;
heavy metal binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.7%; Score 57; DB 23; 100.0%; Pred. No. 4.2e-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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XX PD XX OX XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc which binds mercuric lons. The invention is useful for binds mercuric lons, the invention is a protein in a host-cell, by infecting or transforming a host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing creaming the chelon protein is useful for binding containing the containing heavy metal containing to a solid support, is useful for concentrating heavy metal containing the containing heavy metal consistency, is suitable for use in the in vivo sequestration and containing the containing biological fluids. The nucleic acid, when are encombinantly expressed in enteric bacteria (which are nontoxigenic and containing to to toxic metal ions such as mercury and/or cadmium. The humans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins.

The nucleic acid of the invention is highly specific and binds divalent contains such as mercury and/or cadmium. The nucleic acid of the invention is highly specific and binds divalent the invention are also useful in water treatment resins.

The nucleic acid of the invention is highly specific and binds divalent as mercury or cadmium with high affinity. The present amino cation such as mercury ion binding chelon proteins of the invention.

The invention of the heavy metal binding proteins termed chelons of the invention.
                                                                                                                                                                                                                                                                                                                            В
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2000; 2000US-240465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                 Synthetic cadmium/mercury ion binding chelon protein #4.
                                                                                                                                                               AAU97556;
                                                                                                                                                                                                        AAU97556 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention.
irrigation water; waste stream; contaminated aqueous medium;
                                                                                                                    13-AUG-2002
                     Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                               22 MADLARMETVLSELVCACHARKGNVSCPLIASLOGSSGTHCEEASSLAEHKLKDVRE 78
                                                                                                                                                                                                                                                                                                                          22 MADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVRE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   48.7%; Score 57; DB 23;
100.0%; Pred. No. 4.2e-5:
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117;
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AAU97
                                                                                                                                                                                                                                                                                                                                                                                                                      CC which binds mercuric ions. The invention is useful for recombinantly CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding CC region for the protein to produce a recombinant host cell and culturing CC region for the coding the chelon protein is useful for binding CC The nucleic acid encoding the chelon protein is useful for binding CC metal ions from contaminated soil, ground water, hydroponic solutions or immobilised onto a solid support, is useful for concentrate the heavy in immobilised onto a solid support, is useful for concentrating heavy metal care and environment waste streams or contaminated concentrating heavy metal care recombinantly expressed in enteric bacteria (which are nontoxigenic) and concentration of mercuric ion from gastrointestinal tracts of animals or contaminated to toxic metal ions such as mercury and/or cadmium. The cation such as mercury or cadmium with high affinity. The present amino contaminate acid of the invention is highly specific and binds divalent cation of the heavy ion binding chelon proteins of the invention.

The presents one of the heavy metal binding ordinals termed chelons.
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                    Matches
Synthetic cadmium/mercury ion binding chelon protein #5
                                                                                                                  AAU97557 standard; Protein; 117 AA
                                              13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              or the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                      WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summers AO, Caguiat JJ;
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enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                        48.7%; Score 57;
100.0%; Pred. No
tive 0; Mismato
                                                                                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                                                                                                        DB 23;
. 4.2e-52;
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Qγ

29 ETYLSELYCACHARKGNYSCPLIASLQGSSGTHCEEASSLAEHKLKDYREKMADLAR 85 

Query Match Best Local ( Matches

57;

Conservative

48., 100.08; F1

48.7%; Score 57; DB 23; 100.0%; Pred. No. 4.2e-5; Mismatches

4.2e-52;

Length 117; Indels

o,

Gaps

0,

Similarity

AAU97558

AAU97558 standard; Protein; 117 AA.

AAU97558;

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CC divalent mercuric ions, to take up, sequester and concentrate the heavy content in the invention of content in the invention of content in the invention of irrigation water of waste streams. The DNA of the invention, when content is a solid support, is useful for concentrating heavy metal cons from contaminated environment waste streams or contaminated content in the invention in the invention and content in the invitor sequestration and content in the invention is such as mercury and/or cadmium. The content is acid of the invention are also useful in water treatment resins. Content in such as mercury or cadmium with high affinity. The present amino content is content in the invention is highly specific and binds divalent content content in the invention is highly specific and binds divalent content in the invention is highly specific and binds divalent content in the invention is highly specific and binds divalent content in the invention is highly affinity. The present amino content is content in the invention in the invention in the invention is not the invention.
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                                                      of the invention
                                                            This sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which blinds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding the chelon protein is useful for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-435437/46
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117 AA;
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Synthetic cadmium/mercury ion binding chelon protein

13-AUG-2002 (first entry)

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                                                                                                                                                                                                                                    The nucleic acid encoding the chelon protein is useful for binding contained in the contained and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when commobilised onto a solld support, is useful for concentrating heavy metal consistency may be a solid support, is useful for concentrating heavy metal consistency may be a solid support, is useful for concentrating heavy metal consistency may be a solid support, is useful for concentrating heavy metal consistency may be a solid support, is useful for concentrating heavy metal consistency may be a solid support, is useful for concentrating heavy metal consistency may be a support of metal consistency is suitable for use in the in vivo sequestration and constant of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The consistency metal is sufficient treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino contains such as mercury or cadmium with high affinity. The present amino contains such as mercury or cadmium with high affinity. The present amino contains sequence is one of the heavy metal binding proteins of the invention.
                                                                                      Matches
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   irrigation water; waste stream; contaminated aqueous medium;
biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                            Sequence
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29
                       29 ETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLAR 85
                                                                                                        Local
                                                                                                                                                                                                                        the invention.
ETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLAR
                                                                                      l Similarity
57; Conser
                                                                                                                                                                          117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA molecule comprising a sequence encoding a chelon protein mercuric ions. The invention is useful for recombinantly
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                                                                                                        48.7%;
                                                                                   %; Score 57; DB
%; Pred. No. 4.2
0; Mismatches
                                                                                                             4.2e-52;
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                                                                                        Indels
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                                                                                        Gaps
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AAU97559 ID AAU9

AAU97559 standard; Protein; 117

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48

48 CPLIASLOGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNV 104

104

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RESULT 8

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CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding CC region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC insofting contaminated environment waste streams or contaminated CC ions from contaminated environment waste streams or contaminated CC aqueous medium including biological fluids. The nucleic acid, when CC elimination of mercuric ion from gastrointestinal tracts of animals or CC humans exposed to toxic metal ions such as mercury and/or cadmium. The CC humans exposed to toxic metal ions such as mercury and/or cadmium. The CC cation such as mercury or cadmium with high affinity. The present amino CC cation such as mercury or cadmium with high affinity. The present amino CC cation such as mercury ion binding chelon proteins of the invention. The invention is highly specific and binds divalent coff the invention of the invention. The invention is not of the invention.

CC of the invention of the heavy metal binding proteins termed chelons of the invention.
       Matches
                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 22; 42pp; English.
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                                                                                                                                                    Sequence
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                                         Local
   l Similarity
57; Conserv
                                                                                                                                                                                                                            invention.
                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA molecule comprising a sequence encoding a chelon pro mercuric ions. The invention is useful for recombinantly
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           Conservative
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48.,
100.08; F1
0;
       Score 57; DB; Pred. No. 4.2
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           DB 23; 1
4.2e-52;
hes 0;
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                 acid sequence represents the Shigella flexneri wild type MerR protein of theinvention. This sequence was used in the methods of the invention for production of heavy metal binding proteins termed chelons.
                                                                                                                                                                                                                                                                                                                  nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2000; 2000US-240465P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200230962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irrigation water;
biological fluid;
enteric bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mercuric ion; contaminated soil; ground water; hydroponic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU97551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU97551 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy metal binding
                                                                                                             Local
                   2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 56
2002-435437/46
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK52206
                                                                                                                                                                                            144 AA;
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      waste stream; contaminated aqueous medium; gastrointestinal tract; chelon protein; toxic metal ion; mercury; cadmium; divalent cation; ng protein; MerR.
                                                                                                             100.0%;
                                                                                                                                    47.0%;
                                                                                 0;
                                                                                                                                    Score 55;
                                                                                                             Pred. No.
                                                                              Mismatches
                                                                                                          6.4e-50;
                                                                                                                                 DB 23;
                                                                              0;
                                                                                                                              Length 144
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solution;
                                                                              0;
                                                                         Gaps
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CC recombinant DNA molecule comprising a sequence encoding a chelon protein CC which binds mercuric ions. The invention is useful for recombinantly CC producing a protein in a host-cell, by infecting or transforming a host CC cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC innshilised onto a solid support, is useful for concentrating heavy metal cons from contaminated environment waste streams or contaminated CC aqueous medium including biological fluids. The nucleic acid, when creombinantly expressed in enteric bacteria (which are nontoxigenic and CC elinination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The CC molecules of the invention are also useful in water treatment resins. CC The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino of synthetic cadmium/mercury ion binding chelon proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ХPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNX OXX KW XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-435437/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic cadmium/mercury ion binding chelon protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU97554 standard; Protein; 118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200230962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy metal binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 134
                                                                   sequence is one
                                               invention.
118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                              of the heavy metal binding proteins termed chelons
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Best Local Similarity Matches 48; Conser

Conservative

0;

41.0%;

Score 48; Pred. No. Mismatches

DB 23; 1.2e-42;

Length 118; Indels

0

Gaps

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Query Match

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                                                                 Matches
                                                                              Query Match
Best Local :
                                                                                                                                                         The present sequence represents a protein that is selective towards heavy metal ions. It is used in the construction of the sensor of the invention. The specification describes a metal ion-specific, affinity sensor that measures capacitance. The sensor comprises a piece of noble metal to which are bound groups that bind specifically to selected heavy metal ions. These groups are bound to a self-assembling monolayer that covers at least 90%, more preferably at least 99% of the noble equal surface. The noble metal surface. The noble metal is a rod or piece of insulating material (glass, quartz or silica) on which a noble metal is sputtered. The sensor is used for qualitative or quantitative detection of selected heavy metal ions in liquid samples, particularly of zinc, mercury, coadmium, copper and lead in e.g. environmental samples, medicines,
                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 22-23; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Capacitance sensor specific for heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berggren C, Bontidean I, I
Hobman J, Jakeman K, Johar
Van Der Lelie D, Wilson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-254424/21.
                                                                                                                                                   foods and other products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CSOE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy metal ion selectivity; metal ion-specific affinity sensor; capacitance measurement; noble metal; self-assembling monolayer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09914597-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MerR protein which has selectivity towards heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY01816 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BERG/) BERGGREN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BONT/)
79 GTHCEEASSLAEHKLKDVREKMADLARME 107
                            59 GTHCEEASSLAEHKLKDVREKMADLARME 87
                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mercury; cadmium; copper; lead; environmental sample; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BONTIDEAN I.
CSOEREGI E.
JOHANSSON G.
MATTIASSON B.
MATTIASSON B.
UNIV BIRMINGHAM SCHOOL BIOLOGICAL SCI.
VITO VLAAMSE INSTELLING TECHNOLOGISCH.
                                                                                                                         144 AA;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97SE-0003315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-SE01638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 144 AA.
                                                                        24.8%; Score 29;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johansson G,
                                                            0,
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corbisier P, Csoereg
Lloyd J, Mattiasson
                                                                         DB 20;
. 1.5e-2;
                                                                                      Length 144;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Csoeregi E;
                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                            SON CCC XXX PTT PTT
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AAR49668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA
XX
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
20-JUL-1999; 99EP-0114072.
18-FEB-2000; 2000EP-0103551.
                                  20-JUL-2000; 2000WO-EP06968.
                                                                                 WO200105950-A2.
                                                                                                       Haemophilus influenzae.
                                                                                                                                       Bacteriophage particle; protein display;
                                                                                                                                                                                     08-MAY-2001 (first entry)
                                                           25-JAN-2001.
                                                                                                                           influenza haemagglutinin peptide
                                                                                                                                                             Influenza haemagglutinin peptide
                                                                                                                                                                                                                                   AAY97662 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                The mercury resistance genes can be used as selectable markers when used to transform other bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 2; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-077131/10.
N-PSDB; AAQ58554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP06000083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Resistance; mercury; selectable marker; Thiobacillus ferrooxidans; transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein product of mercury resistance control gene merR(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR49668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR49668 standard; Protein; 159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AKIT-) AKITA KEN.
(DOWA ) DOWA MINING CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                            109 VLSELVCACHARKGNVSCPLIASL 132
                                                                                                                                                                                                                                                                                                                   31 VLSELVCACHARKGNVSCPLIASL 54
                                                                                                                                                                                                                                                                                                                                                                                           159 AA;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91JP-0018338
                                                                                                                                                                                                                                                                                                                                                      20.5%; Score 24;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                      DB 15; ; ; 2.9e-17;
                                                                                                                                                                                                                                                                                                                                                                Length 159;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                          Gaps
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Вp
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The invention relates to a method for displaying a polypeptide/protein on the invention relates to a method for displaying a polypeptide/protein on the guide of the bacteriophage particle. The attachment is via a disulfide bond the bacteriophage particle. The attachment is via a disulfide bond the polypeptide/protein to a unit of the protein coat of the protein coat. Displaying polypeptide/protein and a cysteine coat. Displaying polypeptide/protein on surface of the bacteriophage particle. A collection of the bacteriophage particle is useful for obtaining a polypeptide/protein having a desired property, the collection and/or selecting from a bacteriophage particle to particle to obtain a bacteriophage particle displaying a collection of bacteriophage particle displaying a collection of bacteriophage particles with the target of interest. The method further involves contacting a collection of bacteriophage particles with the target of interest by treating the complexes of target of interest and bacteriophages under reducing conditions. The methods easy creation and screening of large to bacteriophage particles with the target of interest conditions. The methods easy creation and screening of large bacteriophage particles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Displaying polypeptides on bacteriophage surface by attaching the molecules via disulfide bonds formed between cysteine residues present in the polypeptide and cysteine residues in the bacteriophage protein coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-147336/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MORP-) MORPHOSYS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 33; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loehning C,
                                                                                                                                                                                                                                   Adipose protein; adp; obesity; transgenic animal; obesity; adipositas; bulimia; wasting; cachexia; eating disorder; body weight disorder; weight loss; cancer; infectious disease; hypogonadism; Prader-Willi syndrome; Laurence-Moon-Biedl syndrome; hypothyroidism; diabetes; Cushing's syndrome; endocrine disorder; pastrointestinal disease; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                13-JUN-2001; 2001WO-EP06713
                                                          20-DEC-2001
                                                                                                 WO200196371-A2
                                                                                                                                                                                               ulcerative colitis; anorexia nervosa; glycogen storage disease; lipoma; liposarcoma; heart disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                Peptide STREP tag.
                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU80475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU80475 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 SAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SAWSHPOFEK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urban M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                               acquired immunodeficiency syndrome; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 10; DB 22;
100.0%; Pred. No. 0.0012;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knappik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Creamble invention relates to a nucleic acid encoding a adipose (ADP) compositions which regulates, causes or contributes to obesity in an committee of adp activity, adp antisense nucleic acids, expression committees, adp transgenic animals are useful in the diagnosis and contributed to obesity, adipositas, bulimia, wasting (cachexia), eating considers and/or disorders of body weight/body mass, weight loss due to disorders and/or disorders of body weight/body mass, weight loss due to cancer or infectious diseases, genetic disorders associated with hypogonadism, diabetes, Cushing's syndrome, induced the disorders, conjunctions, and anorexia nervosa. They are also useful for treating conditis, and anorexia nervosa. They are also useful for treating compositions are also useful for treating the storage diseases, and lipid storage diseases and for treating lipomas, and/or liposarcomas. The compositions are also useful for treating heart disease, hypertension, and infertility and for treating conditions associated with under weight constraint and munucodeficiency syndrome (AIDS) or cancer patients. The confidence is a peptide tag used in a fusion protein with an account of the confidence of the purification.
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Matches 10
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23-JUN-2000;
28-JUN-2000;
17-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid encoding adipose polypeptide which regulates, causes or contributes to obesity, useful for treating obesity, heart disease, hypertension, infertility, and controlling weight loss in cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 185; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patients
                                                                                                                                                            Streptavidin; purification;
                                                                                                                                                                                                                                                                            AAW59212;
                                                                                                                                                                                                                                                                                                         AAW59212 standard; peptide; 8 AA
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10-OCT-1996;
                                                                                               EP835934-A2
                                                                                                                            Synthetic.
                                                                                                                                                                                                           Streptavidin tagged peptide ligand #2.
                                                                                                                                                                                                                                             27-AUG-1998
                                                              15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         1 SAWSHPQFEK 10
                                                                                                                                                                                                                                                                                                                                                                                                                      SAWSHPQFEK 117
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; 2000EP-0113049.
; 2000US-214518P.
; 2001EP-0109537.
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                                                                                                                                                               recover;
96DE-1041876
                                97EP-0117504.
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100.0%; Pr
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Matches 8; Conserv
                                                                                                                                                                                                                                                                      AAW59211 and AAW59212 are ligands used in a method to assay binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or sensor chips.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to isolate, purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 11; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-218868/20.
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                                                                                                                   110 WSHPQFEK 117
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                                                                                                                                                    6.8%; Score 8; DB 19; Length 8; illarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 2  \$51706  \$51706  \$cpecies: Alcaligenes faecalis  C;Species: Alcaligenes faecalis  C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999  C;Accession: \$51706  R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.  submitted to the EMBL Data Library, May 1994  A;Description: Sequence conservation between regulatory mercury resistance genes from A;Reference number: \$51703  A;Accession: \$51706  A;Status: preliminary A;Molecule type: DNA A;Residues: 1-144 <osb> A;Cross-references: EMBL:Z33484; NID:g607038; PIDN:CAA83892.1; PID:g607039  C;Superfamily: transcription repressor glnR  Query Match Best Local Similarity 100.0%; Pred. No. 4.2e-50; Matches 55; Conservative 0; Mismatches 0; Gaps 0;</osb>	RESULT 1  S09527  regulatory protein merR - plasmid NR1  C; Species: plasmid NR1  C; Species: plasmid NR1  C; Species: plasmid NR1  C; Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 20-Sep-1999  C; Accession: S09527  R; Barrineau, P.; Gilbert, P.; Jackson, W.J.; Jones, C.S.; Summers, A.O.; Wisdom, S. J. Mol. Appl. Genet. 2, 601-619, 1984  A; Title: The DNA sequence of the mercury resistance operon of the IncFII plasmid NR1. A; Reference number: S07447; MUID: 85159407; PMID: 6530603  A; Accession: S09527  A; Mol.ecule type: DNA A; Residues: 1-144 <barn 1-144="" 1-154="" 1-164="" <bar<="" <barn="" a;="" residues:="" th=""><th>30 6 5.1 107 2 B97370 hypothetical prote conserved hypothet 31 6 5.1 117 2 T09740 acceptyl-CoA carboxy 32 6 5.1 127 2 C87640 hypothetical prote 35 6 5.1 156 2 E75218 hypothetical prote 36 6 5.1 162 2 S105712 hypothetical prote 40 6 5.1 177 2 E82306 hypothetical prote 2 S10933 hypoxanthine phosp 39 6 5.1 185 2 D86711 hypoxanthine phosp 30 6 5.1 185 2 D86711 hypoxanthine phosp 30 6 5.1 187 2 T36331 hypoxanthine phosp 30 6 5.1 187 2 T36331 hypoxanthine phosp 30 6 5.1 197 2 T36331 hypoxanthine phosp 30 6 5.1 197 2 T36331 hypoxanthine phosp 30 6 5.1 197 2 T36321 hypothetical prote 30 6 5.1 198 2 G72489 hypothetical prote 30 6 5.1 198 2 G72489 hypothetical prote 30 6 5.1 198 2 G72489 hypothetical prote 30 6 5.1 198 2 G72489</th></barn>	30 6 5.1 107 2 B97370 hypothetical prote conserved hypothet 31 6 5.1 117 2 T09740 acceptyl-CoA carboxy 32 6 5.1 127 2 C87640 hypothetical prote 35 6 5.1 156 2 E75218 hypothetical prote 36 6 5.1 162 2 S105712 hypothetical prote 40 6 5.1 177 2 E82306 hypothetical prote 2 S10933 hypoxanthine phosp 39 6 5.1 185 2 D86711 hypoxanthine phosp 30 6 5.1 185 2 D86711 hypoxanthine phosp 30 6 5.1 187 2 T36331 hypoxanthine phosp 30 6 5.1 187 2 T36331 hypoxanthine phosp 30 6 5.1 197 2 T36331 hypoxanthine phosp 30 6 5.1 197 2 T36331 hypoxanthine phosp 30 6 5.1 197 2 T36321 hypothetical prote 30 6 5.1 198 2 G72489
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A; Reference number: S51703
A; Accession: S51749
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C;Species: Pseudomonas fluorescens
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 24-May-2001
C;Accession: S51749
                                                                                                                                                                  A;Cross-references: EMBL:Z33490; NID:g607153; PIDN:CAA83898.1;
C;Superfamily: transcription repressor glnR
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A; Accession: S51755
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C;Species: Pseudomonas sp.
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
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A;Description: Sequence conservation between regulator
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C;Accession: S51720
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A; Residues: 1-144 < OSB>
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A; Accession: S51720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                      Query Match
                                                                                                                                                      Superfamily: transcription repressor glnR
                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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Best Local :
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                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 DYREKMADLARMETYLSELYCACHARKGNYSCPLIASLQG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTHCEEASSLAEHKLKDVREKMADLARME 107
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                  Similarity
29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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               Conservative
24.8%; 5
100.0%; Pr
0;
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+ ive 0; Mismatches
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100.0%; Pred. No.
                                             Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between regulatory mercury resistance genes from me
                                             DB 2; L
7.5e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                  Length 144;
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           Indels
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           Gaps
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regulatory protein merR - Klebsiella oxytoca
C;Species: Klebsiella oxytoca
C;Date: 07-May-1995 #sequence_revision 01-Se;
                                                                S51705
                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                            C; Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-151 <OSB>
                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: S51721
                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory protein merR - Enterobacter cloacae
C;Species: Enterobacter cloacae
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: merR C;Superfamily: transcription repressor glnR
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S51703
                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z33486; NID: g607073; PIDN: CAA83894.1; PID: g607074
                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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A; Residues: 1-151 <OSB>
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A;Experimental source: isolate SE12
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                          Query Match
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Best Local
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                                                                                                                                          109 VLSELVCACHARKGNVSCPLIASLQ 133
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                                                                                                                                                                            31 VLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                        Focat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 GTHCEEASSLAEHKLKDVREKMADLARME 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.
                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence conservation between regulatory mercury resistance genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                      Conservative
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#sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
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>e: isolate SE11
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100.0%;
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                                                                                                                                                                                                                                      Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25;
Pred. No.
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                                                                                                                                                                                                                    Mismatches
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ches 0;
                                                                                                                                                                                                                                    DB 2; L
1.2e-18;
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Accession: S51705

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A:Cross-references: EMBL:L03729; NID:g1019671; PIDN:AAA98396.1; PID:g154910
A:Experimental source: plasmid Rpl; transposon Tn5053
R:Kholodii, G.Y.; Mindlin, S.Z.; Bass, I.A.; Yurieva, O.V.; Minakhina, S.V.; Nikiforov, Mol. Microbiol. 17, 1189-1200, 1995
A:Title: Four genes, two ends, and a res region are involved in transposition of Tn5053
A:Reference number: S70140; MUID:96130850; PMID:8594337
A:Accession: S70142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Tn5053, a mercury resistance transposon with integron's ends A;Reference number: S32795; MUID:93253772; PMID:8387603 A:Accession: S32798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S32798; S/U142
R;Kholodií, G.Y.; Yurieva, O.V.; Lomovskaya, O.L.; Gorlenko, Z.M.; Mindlin, J. Mol. Biol. 230, 1103-1107, 1993
J. Mol. Biol. 230, 1103-1107.
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A;Title: The sequence of the mer operon of pMER327/419 and transposon ends of pMER327/41
A;Reference number: I39574; MUID:94341572; PMID:8063107
A;Accession: I39574
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R; Osborn,
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-144 <KHO>
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C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999
C;Accession: I39574; S37035
                                               A; Molecule type: DNA
                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       merR protein - Xanthomonas sp. transposon Tn5053
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A; Residues: 1-144 < RES>
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A; Accession: S51705
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z23094; GB:L20693; NID:g388553; PIDN:AAB05979.1; PID:g388554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mer operon regulator -
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A; Residues: 1-151 <0SB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Xanthomonas sp.
;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999
;Accession: S32798; S70142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: transcription repressor glnR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 LYCACHARKGNVSCPLIASLQG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.8%; Score 22; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; L
1.6e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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                                                                                      RESULT 13
S51707
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C; Species:
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                                               regulatory
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N;Alternate names: mer operon regulator
C;Species: Pseudomonas fluorescens
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: EMBL:L40585; NID:g710572; PIDN:AAA98322.1; PID:g710575 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May C;Genetics:
A;Gene: merr
A;Mobile element: transposon Tn5053
C;Superfamily: transcription repressor glnR
                                                                                                                                                            C; Superfamily: transcription repressor glnR
                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-144 < HOB>
                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S37044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z33481; NID:g607169; PIDN:CAA83889.1; A;Note: the source is given as Pseudomonas testosteroni C;Superfamily: transcription repressor glnR
                                                                                                                                                                               A;Cross-references: EMBL:Z23095; NID:g397617; PIDN:CAA80641.1;
                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                  A; \mbox{\it Description:} The nucleotide sequence of the mer operon A; \mbox{\it Reference number:} S37035
                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S51703
A; Accession: S51756
                                                                                                                                                                                                                                                                                                                                                   R;Hobman,
                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S37044
                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory protein merR - Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S37044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-144 < OSB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: Sequence conservation between regulatory mercury resistance genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Osborn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory protein merR - Comamonas testosteroni
C;Species: Comamonas testosteroni
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                                                                                                  Query Match
Best Local
                                                                               Matches
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113 LVCACHARKGNVSCPLIASLOG
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                                    35 LVCACHARKGNVSCPLIASLQG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LVCACHARKGNVSCPLIASLOG 56
                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 LYCACHARKGNYSCPLIASLQG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                              Kholodii, G.; Nikiforov, V.; Ritchie, D.A.; Strike, P.; Yurieva,
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                18.8%; Score 22; 100.0%; Pred. No.
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; Pred. No.
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                                                                                                                      DB 2;
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                                                                                                                   Length 144;
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                                                                             Indels
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protein merR - Agrobacterium Agrobacterium radiobacter

radiobacter

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C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C;Accession: S51707
R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.
submitted to the EMBL Data Library, May 1994
A;Description: Sequence conservation between regulatory mercury resistance genes from material A;Reference number: S51703
A;Accession: S51707
                                                                                                                                                                                                                                                                                                                                                                                                              50S ribosomal chain protein L28 [imported] - Salmonella enterica subsp. enterica serova. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002 C;Accession: AE0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           merR protein - Escherichia coli plasmid pDU1358
C;Species: Escherichia coli
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-151 <OSB>
                                                                                                                                                                                     , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: transcription repressor glnR
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Mercury operon regulation by the merR gene of the organomercurial resistance A;Reference number: A33858; MUID:89327136; PMID:2666393 A;Accession: A33858
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R;Nucifora, G.; Chu, L.; Silver, S.; Misra, T.K.
J. Bacteriol. 171, 4241-4247, 1989
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A;Cross-references: GB:AL513382; PIDN:CAD03265.1; PID:g16504886; C;Genetics: A;Gene: ST$4.066
C;Superfamily: Escherichia coli ribosomal protein L28
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A; Residues: 1-144 < NUC>
                                                                                                              A; Molecule type: DNA
A; Residues: 1-78 < PAR>
                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                   R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M24940; NID:g150631; PIDN:AAA98221.1; PID:g455313
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Db 65 ETVLSEL 71
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Search completed: May 28, 2003, 10:42:29 Job time: 45 secs

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Result
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Maximum DB seq length: 2000000000
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FKB3_RABIT
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202.197 Million cell
p07044 salmonella
p07044 salmonella
p16688 pseudomonas
p13111 serratia ma
o54325 salmonella
o54325 salmonella
p27192 escherichia
o52948 rhizobium m
p58708 ralstonia s
p15307 mus musculu
o52452 pseudanabae
p14876 fremyella d
p18134 vibrio harv
o9ms97 galdieria s
o9chn6 lactococcus
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o9chn6 lactococcus
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o9chn6 lactococcus
p27740 rhodobacter
o50412 magnetospii
o29208 archaeogloi
p87495 carassius ;
p09585 cyprinus c.
p29235 hypophthali
p57356 buchnera a
o9wuz7 mus muscul
p37678 escherichi
o46638 oryctolagu
p26884 bos taurus
o00688 homo sapis
o62446 mus muscul
o41274 sinapis a.
o445577 bacillus ;
p35256 marburg v
p31315 mus muscul
o9v4q8 drosophil
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Matches 55
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR. FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric resistance;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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METAL
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TRANSPOSON-Tn501;
MEDLINE-85014891; PubMed-6091128;
                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                           Osborn A.M.,
                                                                                                                                                                                                                                                                        STRAIN=SB4;
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                                                                                                                                                                                                                                                                                                              "Mercuric ion-resistance operons of plasmid R100 Tn501: the beginning of the operon including the and the first two structural genes."
Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas
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                                                   SIMILARITY:
                                                                          RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE IC AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAIN:
                                         REGULATORS.
                                                                   BOUND TO THE MER SITE.
                                                                                                                                    FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY
SWISS-PROT entry is copyright.
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K03089; AAB59072.1; -.
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                                                                                                                                                                                                                                             M., Bruce K.D., Strike P., Ritchie D.A.;
(DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                      BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   294;
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82
117
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                                                   TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory protein
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Pred. No.
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HG(2+).
HG(2+).
HG(2+).
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                                                                              REMAINING
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            collaboration
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RESULT 3
MERR_SERMA
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                                                                                                                                                NUCIFORA G., Chu L., SILVER S., MISRA T.K.;

"MERCURY OPERON regulation by the merr gene of the organomercurial resistance system of plasmid pDU1358.";

J. Bacteriol. 171:4241-4247 (1989).

-I- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PL311;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Mercuric resistance operon regulatory protein.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric Mercury; DNA-binding; Plasmid; Transposable element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z00027; CAA77320.1; -. EMBL; Z33489; CAA83897.1; -. EMBL; Z33490; CAA83898.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-89327136; PubMed-2666393;
                                                                                                                                                                                                                                                                                                                                                                                                                                Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pDU1358
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Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serratia marcescens.
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                                                                                       REGULATORS.
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                                                                                                          MER SITE.
BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
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100.0%;
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Pred. No
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HG(2+)
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C->A: ABOLISHES TRANSCRIPTIONAL
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C573298AFF0846EF CRC64;
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Pfam; PF00376; merR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-S.typhimurium; STRAIN-LTZ:
MEDLINE-98055334; PubMed-9393616;
Suzuki M., Matsui K., Yamada M., Kasai H., Sofuni T., Nohmi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium, and
Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50S ribosomal protein L28. RPMB OR STM3728 OR STY4066.
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                                                                                                                                                                                                                                              McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                            "Construction of mutants of Salmonella typhimurium deficient in 8-hydroxyguanine DNA glycosylase and their sensitivities to oxidative mutagens and nitro compounds.";
Mutat. Res. 393:233-246(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  054335;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALTY
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           SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; Wain J
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J
Churcher C., Mungall K.D., Bentley S.D., Holden M.T., Connerton P.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Cronin A., Davis P., Davies R.M., Holm T.T., Holtoyd S., Jagels K.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holtoyd S., Jagels K.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holtoyd S., Jagels K.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holtoyd S., Jagels K.,
                                                                                                                                                                                                                                                                                                                     SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 Waterston R., Wilson R.K.;
                                                                                                                                                                               Nature 413:852-856(2001).
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Larsen T.S., Leather S., Moule S., O'Gaora P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 AA;
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HG (2+)
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Pred. No.
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  TRD5_ECOLI
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P27192;
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U23405; AAC01771.1; -. EMBL; AE008873; AAL22587.1; -. EMBL; AL627280; CAD03265.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quail M., Rutherford K., Simmonds M., Skelton J., Stevens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitehead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00830; Ribosomal_L28; 1.
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EMBL;
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miele L., Strack B., Kruft V., Lanka E.;
"Gene organization and nucleotide sequence of the primase region IncP plasmids RP4 and R751.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid IncP-beta R751
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                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases -i- SIMILARITY: TO PLASMID INCP-ALPHA RP4 TRAD.
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                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                               Thomas C.M.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92297959; PubMed=1818755;
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  X59794; CAA42459.1;
U67194; AAC64471.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001383; Ribosomal_L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23, Created)23, Last sequence update)41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8919 MW;
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100.0%; Pr
                                                                                                                                                           rmatics Institute. There are no rest institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lanka E.;
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                                                                                                            (See http://www.isb-sib.ch/announce,
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                                                                                                                                     Usage
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FLGI_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                  CONFLICT
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    InterPro; ipR001782; Flag_FlgI.
Pfam; pF02119; FlgI; 1.
PRINTS; PR01010; FLGPRINGFLGI.
                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Botstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLGI_RHIME
Q52948;
    SEQUENCE
                  CONFLICT
                                                                 CHAIN
                                                                             SIGNAL
                                                                                                                                                    EMBL; L49337; AAB81415.1; -.
EMBL; AL591784; CAC45236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update)
Flagellar P-ring protein precursor (Basal body P-ring protein).
FLGI OR R00664 OR SMC03032.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S37
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-RU11/001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 VREKMAD 38
                                                                                                                                                                                                                                                                                                                      SUBGELLULAR LOCATION: Periplasmic (By similarity).
                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE FLGI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE L-RING AND PROTECTS THE MOTOR/BASAL BODY FROM SHEARING FORCES DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S37670; S37670.
                                                                                           Periplasmic;
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7
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   38357 MW;
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100.0%; Pred. No.
                                                                                         Signal;
               N -> K (IN REF. 1)
V -> A (IN REF. 1)
G -> GR (IN REF. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                             FLAGELLAR P-RING PROTEIN
N -> K (IN REF. 1).
V -> A (IN REF. 1).
                                                                        POTENTIAL.
06BB4E95EE029100 CRC64;
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Best Local Similarity
7; Conserve
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Best Local
                                                                                                                                                                                               Matches
                     01-APR-1990 (Rel. 14, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
C-Rel proto-oncogene protein (C-Rel protein)
                                                                       REL_MOUSE P15307;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PRINTS; PR00084; MTLDHDRCNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; FALSE_NEG.
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                      Oxidoreductase;
                                                                                                                                                                                                                                                                                                                     EMBL; AL646068; CAD15836.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21681879; PubMed=11823852;
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
D-arabinitol 4-dehydrogenase (EC 1.1.1.11).
                                                                                                                                                 203
                                                                                                                                                                        103 NVSCPSA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=305;
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                                                                                                                                                                                                         Local
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                                                                                                                                               NVSCPSA 209
                                                                                                                                                                                               Similarity
7; Conser
                                                                                                                                                                                                                                              465 AA;
                                                                                                                                                                                               Conservative
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                                                                                   STANDARD;
                                                                                                                                                                                                                                                       NAD;
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100.0%; Pred. No.
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                   Length 465;
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Mus musculus (Mouse).

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                                                                                                                                                               RESULT 9
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Best Local (
                                                       РНА2_PSEA9 STANDARD;
Q52452;
Q1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last ann
C-phycocyanin-2 alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grumont R.J., Gerondakis S.;
"The murine c-rel proto-oncogene encodes two mRNAs the expression of which is modulated by lymphoid stimuli.";
Oncogene Res. 5:245-254(1990).
-I- FUNCTION: PROTO-ONCOGENE THAT MAY PLAY A ROLE IN DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grumont R.J., Gerondakis S.; "Structure of a mammalian c-rel protein deduced from the nucleotide sequence of murine cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Spleen;
MEDLINE=89239482; PubMed=2654811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002909; IPT_TIG.
InterPro; IPR00451; NF_Rel_dor_fam.
Pfam; PF00554; RHD; 1.
Pfam; PF01833; TIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A45505; A45505.
PIR; A60367; A60367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X15842; CAA33843.1; ALT_SEQ. EMBL; X60271; CAA42817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90370373; PubMed=2204017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene Res. 4:1-8(1989)
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01204; REL_1; 1.

PROSITE; PS01254; REL_2; 1.

Proto-oncogene; Phosphorylation; Nuclear protein.

DOMAIN 8 297

REL-LIKE (RHD).
                 Bacteria; Cyanobacteria; Oscillatoriales; Pseudanabaena
                                              CPCA2
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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NCBI_TaxID=29415;
                             Pseudanabaena sp.
                                                                                                                                                                                                          440 DLARMET 446
                                                                                                                                                                                                                                    24 DLARMET 30
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SM00429; IPT; 1.
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267
587 AA;
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                             (strain PCC 7409)
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100.0%; F1
                                                                                                                                                                                                                                                                                                                           64960 MW;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                         REL-LIKE (RHD).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PKA) (POTENTIAL).
98FC237B6D140416 CRC64;
                                                                                                                                 PRT;
                                                                                                                                    162 AA
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PHA3_FREDI
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Best Local :
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P14876;
Ol-APR-1990 (Rel. 14, Created)
Ol-APR-1990 (Rel. 14, Last sequence up
Ol-JUL-1993 (Rel. 26, Last annotation
C-phycocyanin-3 alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dubbs J.M., Bryant D.A.;
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.

SIDDITTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT
FROM THE PHYCOBILLPROTEIN COMPLEX.

-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M99427; AAA26044.1; -. HSSP; P07122; 1CPC. InterPro; IPR001659; Phycobilisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mazel D., Houmard J., Tandeau de Marsac N.;
"A multigene family in Calothrix sp. PCC 7601 encodes phycocyanin, the major component of the cyanobacterial light harvesting antenna.";
Mol. Gen. Genet. 211:296-304(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
BINDING 84
SEQUENCE 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                           This
                                                                                                                                                                   Mazel D., Marilere P.;
"Adaptive eradication of methionine and cysteine from cyanobacterial light-harvesting proteins.";
Nature 341:245-248(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=89384903; PubMed=2506452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPCA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1197;
                                                                                                                                                                                                                                                                                                        -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
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                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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100.0%; Pred. No.
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17301 MW;
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BILE PIGMENT-PROTEIN
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MBL outstation -
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VIBHA
HPRT_VIBHA
11...

P18134;

01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                            InterPro; IPR000836; PRTransferase.
InterPro; IPR002375; Pr/py_rp_transf.
Pfam; PF00156; Pribosyltran; 1.
TIGRRAMS; TIGR01203; HGPRTase; 1.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
                                                                                                                                                                                   EMBL; X53382; CAA37462.1; -. PIR; S10993; S10993. HSSP; Q26997; 1QK3.
                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:4621-4621(1990).
-I- FUNCTION: THIS ENZYME ACTS EXCLUSIVELY HYPOXANTHINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90356428; pubMed-2388850;
Showalter R.E., Silverman M.R.;
"Nucleotide sequence of a gene, hpt, for hypoxanthine
phosphoribosyltransferase from vibrio harveyi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio harveyi.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phycobilisome; Electron transport; Photosynthesis; Bile pigment; Multigene family.
BINDING 84 84 PHYCOCYANOBILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X06083; CAA29460.1; -.
PIR; S05712; S05712.
HSSP; P07122; ICPC.
InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: IMP + diphosphate =
                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-D-ribose 1-diphosphate.
PATHWAY: Purine salvage.
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                                  AΑ;
                                  19963 MW;
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17392 MW;
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MAGNESIUM (BY SIMILARITY).
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Score 6;
                               2027D73A9CAAAACE CRC64;
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39;
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Length 176;

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OSSEDDEDE
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                                                                                                                                                          RESULT 13
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Best Local :
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                                                                                                                                       LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C_GALSU
IF3C_GALSU
Q9MS97;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                        Q9CHN6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elongation factor P (EF-P).
Lactococcus lactis (subsp. lactis) (Streptococcus lactis). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE EQUILIBRUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN FAVOR OF THE FREE SUBUNITS, THUS EMHANCING THE AVAILABILITY OF 30S SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
                                                                                                                          EFP_LACLA
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00707; IF3; 1.
ProDom; PD002880; IF3; 1.
TIGRFAMS; TIGR00168; infC; 1.
PROSITE; PS00938; IF3; 1.
                                                                                                                                                                                                                                                                                                                                Initiation factor; Protein biosynthesis; Chloroplast.
SEQUENCE 181 AA; 21393 MW; 572014236DE7ABF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001288; IF3. Pfam; PF00707; IF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF233069; AAF81685.1; -. HSSP; P03000; ITIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-UTEX 2393; Whitney S.M., And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galdieria sulphuraria Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Translation initiation factor IF-3, chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galdieria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=130081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFC OR IF3
                                                                                                                                                                                                       156 SSLAEH 161
                                                                                                                                                                                                                                      66 SSLAEH 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 MADLAR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE IF-3 FAMILY.
                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrews J.;
                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                 %; Score 6; DB 1
%; Pred. No. 43;
0; Mismatches
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                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                          185 AA
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                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                Length 181;
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Lactococcus.
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RESULT 14
DCTR_RHOCA
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                                                                                                       Hamblin M.J., Shaw J.G., Kelly D.J.;
"Sequence analysis and interposon mutagenesis of a sensor-kinase (DctS) and response-regulator (DctR) controlling synthesis of the high-affinity C4-dicarboxylate transport system in Rhodobacter capsulatus.";
                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001059; EF-P.
Pfam; PF01132; EFF; 1.
TIGRFAMs; TIGR00038; efp; 1.
PROSITE; PS01275; EFP; 1.
Protein biosynthesis; Elongation factor; Complete proteome.
Protein biosynthesis; Elongation factor; Complete proteome.
                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 33303 / B10;
MEDLINE-93204897; PubMed-8455557;
                                                                                                                                                                                                                                                                                                         Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                              C4-dicarboxylate transport transcriptional regulatory protein dctR.
                                                                                                                                                                                                                                                                                                                                                                                                                                       P37740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCTR_RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
                                                                                                                                                                                                                                                                         NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                              Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE006302; AAK04790.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21235186; PubMed=11337471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 KLKDVR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                    FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR INVOLVED IN THE TRANSPORT OF C4-DICARBOXYLATES. DCTR FUNCTIONS AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE (BY
                  A TRANSCRIPTIONAL REPRESSOR OF GENES TRANSPORT.
SUBCELLULAR LOCATION: Cytoplasmic (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: Protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                          Gen. Genet. 237:215-224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                   FOR C4-DICARBOXYLATE
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RNH2_MAGSA
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Best Local
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Pfam; PF00078; GerE; 1.
PRINTS; PR00038; HTHLUXR.
ProDom; PD000039; Response_reg; 1
ProDom; PD000307; HTH_LuxR; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                RNH2_MAGSA STANDARD S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
SEQUENCE
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                                                                                                                                                                     PROSITE; PS00622; HTH_LUXR_FAMILY; 1. PROSITE; PS50110; RESPONSE_REGULATORY; Sensory transduction; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- SIMILARITY: CONTAINS 1 RESP
-i- SIMILARITY: BELONGS TO THE 1
REGULATORS.
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement
                                                                                                            phosphomonoester.
-!- COFACTOR: MANGANESE (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: Cytoplasmic (
                                                                                                                                                                                                                                                                                                                                                                                                                 Magnetospirillum sp. (stra Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64733; CAA46000.1; -.
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                                                                                        -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                     STRAIN-AMB-1;
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=84159;
                                                                                                                                                                                                                                                                                                                                                                                                Magnetospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activator; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000792; InterPro; IPR001789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S30289; S30289.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 ADLARM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ADLARM 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P10958; 1DBW.
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128
160
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (strain AMB-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                   alpha subdivision; Rhodospirillaceae;
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THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
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Pred. No.
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PHOSPHORYLATION (BY SIMILARITY)
INTER-DOMAIN LINKER (POTENTIAL)
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    Transcription regulation;

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European

Bioinformatics

Institute.

There

are no

restrictions

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CC use by non-profit institutions as long as its content is in no way cc modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).

CR EMBL: D32253; BAA06983.1; -...

DR HSSP; Q57599; LEKE.

DR HSSP; Q57599; LEKE.

DR HSSP; Q57599; LEKE.

DR Hydrolase; Nuclease; Endonuclease; Manganese.

FT ACT_SITE 18 18 BY SIMILARITY.

FT ACT_SITE 113 113 BY SIMILARITY.

FT ACT_SITE 113 113 BY SIMILARITY.

SQ SEQUENCE 201 AA; 21597 MW; OD01B23CF85DD2A2 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qu 22 MADLAR 27

Qu 22 MADLAR 27

Qu 22 MADLAR 157

Search completed: May 28, 2003, 10:40:07

Job time: 26 secs
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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
 112
113
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115
                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-977-137A-4
                                                                                                                                                               Match
                                                                                                                                                                         Query
SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              sp_phage: *
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                                                                                                                                                                                                                                                                                                                                                                              sp_human:*
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                                                                                                                                                                                                                                                                    sp_unclassified:*
sp_rvirus:*
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172
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        Q9r9w9 pseudomonas
Q60233 alcaligenes
Q934s8 thiobacillu
Q44191 agrobacteri
Q99093 acinetobact
Q995515 salmonella
                                                               Q8rk29 pseudomonas
Q44190 alcaligenes
Q4655 enterobacte
Q9r9x0 pseudomonas
Q52395 pseudomonas
Q52395 pseudomonas
Q52492 enterobacte
Q7304 pseudomonas
Q57106 acinetobact
                                                                                                                                                              Description
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į	Д,	44	43	42	41	40	39	38	37		35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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*	08WH74	019129	Q9KNHO	030342	Q69007	ש	004137	0	P74440	o		Q9ESK6	Q9QX02	Q9UGE2	Q9QX12	Q9ET81	Q9VCB8	Ø									Q99092	0	P77071
	08wh74 frasera tub	019129 bos taurus		030342 vibrio chol	7 human	S	7 med	ъ	P74440 synechocyst	09vbu7 drosophila	σ			Q9uge2 homo sapien	Q9qx12 rattus norv	Q9et81 rattus norv	Q		Q9sak7 arabidopsis					Q9hh01 pyrococcus	Q9y9h7 aeropyrum p	Q975q0 sulfolobus	Q99092 acinetobact		p77071 escherichia

#### ALIGNMENTS

RESULT 1

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RESULT 2
Q44190
ID Q441
AC Q441
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                                                                                        δõ
                                                                                                                                                           Q8RK29
                                                                                                                Matches
                                                                                                                                   Query Match
 Q44190
Q44190;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                           Q8RK29
                                                                                                                                                                                                                                                                                                                                                    MerR protein (Fragment).
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                 Plasmid.
                                                                                                                                                                                           EMBL; AJ422225; CAD19592.1;
                                                                                                                                                                                                        Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                   bacteria
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TRANSPOSON-TN21 HOMOLOGUE;
Kholodii G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
"Distribution of distinct microvariants of Tn5041 in environmental
                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                  Plasmid pKLH22.
                                                                                                                                                                                                                                                                                                                             Pseudomonas fluorescens.
                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                  NCBI_TaxID=294;
                                                                 Local Similarity
                                                                                                                                                           124 AA; 13759 MW;
                                                                                                               47.0%; Score 55; DB 2; Lilarity 100.0%; Pred. No. 1.8e-50; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
               PRT;
                                                                                                                                                            C514222BB0ED7754 CRC64;
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               144 AA
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                                                                                                                                    Length 124;
                                                                                                                Indels
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007300 pseudomonas

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-T238;
OSborn A.M., Bruce K.D., Strike P., Ritchie D.A.;
OSborn A.M., Bruce K.D., Strike P., Ritchie D.A.;
"Sequence Conservation between Regulatory Mercury Resistance Genes
"Sequence Conservation between Regulatory Mercury Resistance Genes
from Mercury Polluted and Pristine Environments.";
from Mercury Polluted and Pristine Environments.";
Substituting Training T
                                                                                                                                                                                                       PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS000552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 144 AA; 15652 MW; 1D6E1F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q46655
Q46655;
Q1-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osborn A.M., Bruce K.D., Strike P., Kilcuis J...., Osborn A.M., Bruce K.D., Strike P., Kilcuis J...., Resistance "Sequence Conservation between Regulatory Mercury Resistance from Mercury Polluted and Pristine Environments."; from Mercury Polluted and Pristine Environments."; Gatabases.
                                                                                                                                                                                                                                                                                                                                                               REGULATORS.
EMBL; Z33488; CAA83896.1; -.
InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000551;
Pfam; PF00376; merR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z33484; CAA83892.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes faecalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=548;
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   17 DVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 134
                                                                                                                            Similarity
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ing; Transcription regulation
144 AA; 15832 MW; B71D7FF
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                      100.0%;
                                                                                                                                                        34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTH_MerR.
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Last annotation update
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                                                                                                                                                                                                             1D6E1F50D37A1337 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MERR FAMILY OF TRANSCRIPTIONAL
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                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144
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. 2e-50;
                                                                                                                                                        DB 2;
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                                                                                                                         .7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                  Length 144;
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                                                                                             Indels
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                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
   ACCOMPANDA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q52395
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Q52395;
Proc.
                                                                                                                                            SPECIES-P.stutzeri; STRAIN-OX; PLASMID-PPB;
MEDLINE-85014891; PubMed-6091128;
Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D.,
Haberstroh L., Silver S.;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SPECIES-P.putida; PLASMID-PWWO;

Greated A., Lambertson L., Williams P.A., Thomas C.M.;

Grouplete nucleotide sequence of IncP-9 plasmid pwwO.";

"Complete nucleotide sequence" ("Thomas C.M.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                 "Mercuric ion-resistance operons of plasmid R100 and transposon the beginning of the operon including the regulatory region and first two structural genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida, and Pseudomonas perfectomarina).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MERR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative MerR protein (Organomercurial resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pWW0, and Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "mer sequences on plasmids.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092069; AAD52705.1;
InterPro; IPR000551; HTH_MerR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid group 2 plasmid.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9R9X0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00422; HTH_MERR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruce K.D., Lilley A.K., Bailey M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-KT2440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 DVREKMADLARMETVLSELVCACHARKGNVSCPLI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                        Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
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35; Conserv
                                                                                                                                                                                                                                                                                                                                (AUG-2001) to
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316;
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                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
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Barnes W.M.,

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                                                                                                                                                                                                                                                                                                   RESULT 6
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                                                                                                                   Shigella flexneri.
Plasmid virulence plasmid pWR501.
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                     Q9AFK4;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0040; HTHMERR.

SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

Plasmid; DNA-binding; Transcription regulation.

Plasmid; DNA-binding; T5884 MW; F5760BEC8860ZFC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATORS.
EMBL; AJ344088; CAC86844.1; -.
EMBL; U90263; AAC38229.1; -.
InterPro; IPRO00551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86174347; PubMed=3007931; Brown N.L., Misra T.K., Winnie J.N., Schmidt A., Seiff M., Silver S.; Brown N.L., Misra T.K., Winnie J.N., Schmidt A., Seiff M., Silver S.; The nucleotide sequence of the mercuric resistance operons of plasmid R100 and transposon Tn501: further evidence for mer genes which enhance the activity of the mercuric ion detoxification system."; Mol. Gen. Genet. 202:143-151(1986).
                                                                                                                                                                         MERR.
                                                                                                                                                                                      In501 repressor.
                                                                                                                                                                                                                                                                       Q9AFK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96105204; PubMed-8529897;
Reniero D., Galli E., Barbieri P.;
"Cloning and comparison of mercury- and organomercurial-resistance determinants from a Pseudomonas stutzeri plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-P. stutzeri; STRAIN-OX; PLASMID-PPB;
MEDLINE-9353772; PubMed-8387603;
Kholodii G.Ya, Yurieva O.V., Lomovskaya O.L.,
Mindlin S.Z., Nikiforoy V.G.;
                                           SEQUENCE FROM N.A. MEDLINE=21189246; PubMed=11292750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98148002; PubMed-9479042;
Renlero D., Mozzon E., Galli E., Barbieri P.;
"Two aberrant mercury resistance transposons in the Pseudomonas
stutzeri plasmid pPB.";
              Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J.,
Blattner F.R.;
                                                                                           NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=P.stutzeri; STRAIN=OX; PLASMID=PPB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 166:77-82(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Tn5053, a mercury resistance transposon with integron's ends.";
J. Mol. Biol. 230:1103-1107(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=P.stutzeri; STRAIN=OX; PLASMID=PPB;
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Complete DNA sequence and analysis of the large virulence plasmid of
                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                 59 GTHCEEASSLAEHKLKDVREKMADLARME 87
                                                                                                                                                                                                                                                                                                                                                                                                                             ocal
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                                                                                                                                                                                                                                                                                                                                                    GTHCEEASSLAEHKLKDVREKMADLARME 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208:37-42(1998)
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29; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                               24.8%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             score 29; DB; Pred. No. 7.9
                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                       172
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7.9e-23;
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                                                                                                                           Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 144;
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RESULT 8
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PAC PAC
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Matches
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Best Local 9
                     007304;
                                                                                                                                                                                      PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16559 MW; 238460F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q57492
Q57492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLIEL 01, 01-NOV-1996 (TREMBLIEL 01, 01-JUN-2001 (TREMBLIEL 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0040; HTHMERR.

SMART; SM00422; HTH_MERR; 1.

PROSTITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Plasmid; Transcription regulation.

DNA-binding; Plasmid; Transcription regulation.

SEQUENCE 172 AA; 18826 MW; 897D139E7BC182A9 CRC64;
                                                                                                                                                                                                                                                      EMBL; Z33486; CAA83894.1; -.
EMBL; Z33485; CAA83893.1; -.
EMBL; Z33485; CAA83894.1; -.
InterPro; IPRO00551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella oxytoca.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000551; H
Pfam; PF00376; nerR; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigella flexneri.";
Infect. Immun. 69:3271-3285(2001).
-!- SIMILARITY: BELONGS TO THE MER
                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1994) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                         Osborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                   Osborn A.M., Bruce K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SO1;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacter cloacae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                      STRAIN-SE31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=550, 571;
                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 GTHCEEASSLAEHKLKDVREKMADLARME 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                     31 VLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGULATORS
                                                                                                                                                                                                                                                                                                       REGULATORS.
                                                                                              VLSELVCACHARKGNVSCPLIASLQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTHCEEASSLAEHKLKDVREKMADLARME 87
                                                                                                                                              l Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.8%; Score 29;
illarity 100.0%; Pred. No.
Conservative 0; Minner
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                   PRELIMINARY;
                                                                                                                                                       21.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ TO THE MERR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                     Strike P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                   Score 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                              238460FCE51754AD CRC64;
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                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Ritchie
                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Lo
                                                                                                                                                        1.5e-18;
                                   B
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                                                                                                                                                                                                                                                                                                                   databases.
TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                   Length 151;
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                                                                                                                                              Gaps
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01-JUL-1997 01-NOV-1999

(TrEMBLrel.

04, 12,

Last sequence update)

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RESULT

Q57106

ID 705

AC Q55

AC Q5

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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     057106 PRELIMINARY; PRT; 151 AA.

957106; O08282; O08130; O08287; O08166; O08288; O08185;
01-NOV-1996 (TrembLrel. 01, Created)
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-DEC-2001 (TrembLrel. 19, Last annotation update)
Regulatory protein (Mercury resistance operon regulatory protein) (MER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0040; HTHMERR.

SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription regulation.

SEQUENCE 151 AA; 16541 MW; 17CC8F1005A33FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas sp.
Bacteria; Proteobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MERR protein (Mercuric resistance operon regulatory protein).
                                                                                                                                                                                                                                                                                                                                        Acinetobacter sp., and Acinetobacter sp. LS56-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y09210; CAA70409.2; -. EMBL; Y19976; CABBL5701.1; -. InterPro; IPR000551; HT_Meri Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yurleva O., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E., Mindilin S., Nikiforov V.; "Intercontinental spread of promiscuous mercury-resistance transposons in environmental bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Submitted (DEC-1994) [2]
                                                                                                                                                                                                                                                                         Acinetobacter.
                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russ. J. Genet. 36:365-3
                                                                           Osborn A.M.,
                                                                                                          STRAIN-SE12;
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                             NCBI_TaxID=471, 562, 512,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pantoea agglomerans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acinetobacter calcoaceticus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kholodii G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 24:321-329(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97303088; PubMed=9159519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kholodii G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular genetic analysis of the Tn5041 transposition system."; \alpha vss. J. Genet. 36:365-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ikiforov V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  و
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y., Mindlin S.Z., Gorlenko Z.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                       Bruce K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTH_MerR.
                                   ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ţ
                       , Strike P., Ritchie D.A.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ю
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                                                                                                                                                                                                                                 549,
                                                                                                                                                                                                                                                                                                         gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 25; DB
%; Pred. No. 1.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                 550,
                                                                                                                                                                                                                                                                                                     subdivision; Moraxellaceae;
                                                                                                                                                                                                                                 472, 107402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bass I.A., Kalyaeva E.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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RESULT 10
Q9R9W9
     DE RECEPTION OF THE PROPERTY O
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y09026; CAA70240.1; -.
EMBL; X08993; CAA70195.1; -.
EMBL; Z33483; CAA83891.1; -.
EMBL; Z33482; CAA83890.1; -.
EMBL; Y08992; CAA70185.1; -.
EMBL; Y08992; CAA70237.1; -.
EMBL; A7245842; CAC80722.1; -.
EMBL; A7245866; CAC38823.1; -.
EMBL; A7250860; CAC38823.1; -.
EMBL; A726860; CAC38823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                O9R9W9;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0040; HTHMERR.

SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Plasmid; Transcription regulation.

DNA-binding; Plasmid; Transcription regulation.

SEQUENCE 151 AA; 16529 MW; 239350FCE51754AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CH210; TRANSPOSON-TN5059;
MEDLINE-97303088; PubMed-9159519;
Yurieva O., Kholodii G., Minakhin L.,
Mindlin S., Nikiforov V.;
"mer sequences on plasmids."
Submitted (SEP-1998) to the
EMBL; AF092070; AAD52706.1;
                                                                           SEQUENCE FROM N.A.
STRAIN=KT2440;
Bruce K.D., Lilley A.K.,
                                                                                                                                                                                                                                          Pseudomonas putida.
Plasmid group 5 plasmid.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-Acinetobacter sp. LS56-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "pKLH2-like aberrant transposons and possible mechanisms dissemination.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Acinetobacter sp.; STRAIN=BW3; PLASMID=PKLH207; TRANSPOSON=TNPKLH207 INPKLH2-LIKE ABERRANT TRANSPOSON; Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.
                                                                                                                                                                                                                                                                                                                                                 MerR (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R9W9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The shuffling function of Gene 269:121-130(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nikiforov
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                                                                                                                                                                                        NCBI_TaxID=303;
                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kholodii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSPOSON-TNPKLH204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 VLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLSELVCACHARKGNVSCPLIASLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%; 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                              Bailey M.J.;
                                                                                                                                                                                                                                             gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resolvases.";
                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID-PKLH204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                update)
                              databases
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QGC 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q60233 PRELIMINARY; PRT; 144 AA.
Q60233; P75015; Q44314; Q51768; Q51808; Q52601; Q56390; Q56443;
Q1-NOV-1996 (TremBLrel. 01, Created)
Q1-NOV-1996 (TremBLrel. 01, Last sequence update)
Q1-MAR-2002 (TremBLrel. 20, Last annotation update)
Mercuric resistance operon regulatory protein (MERR protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comamonas testosteroni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alcaligenes sp.,
Pseudomonas fluorescens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00422; HTH_MERR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of the mer operon of pMER327/419 and transposon ends pMER327/419, 330 and 05."; Gene 146:73-78(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-Alcaligenes sp., and P.fluorescens; TRANSPOSON-TN5053; MEDLINE-94341572; PubMed-8063107; Hobman J., Kholodii G., Nikiforov V., Ritchie D.A., Strike P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas sp. (strain ADP).
Plasmid pMER327, Plasmid RP1, and plasmid pADP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified,
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                    SPECIES=Xanthomonas; PLASMID=RPI; TRANSPOSON=TN5053; MEDLINE=93253772; PubMed=8387603; Kholodii G.Ra., Yurieva O.V., Lomovskaya O.L., Gorlenko Zh.M., Mindlin S.Z., Nikiforov V.G.; "Tn5053, a mercury resistance transposon with integron's ends."; Mol. Biol. 230:1103-1107(1993).
                                                                                                                                                                                                                                                                                                                                                                                              "Four genes, two ends, and a res region are involved in transposition of Tp5053: a paradigm for a novel family of transposons carrying either a mer operon or an integran."; Mol. Microbiol. 17:1189-1200(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96130850; PubMed=8594337;
Kholodii G.Y., Mindlin S.Z., Bass I.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xanthomonas, and
                                                                                                                                                                                                                                                                                                                SPECIES=unidentified;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=unidentified;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=C.testosteroni; STRAIN=SE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        Kholodii
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ľurieva O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                           Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
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                                                                                                                                                                                                                                                              31:1447-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2C7C09EE8ACB7BCA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yurieva O.V., Minakhina S.V.,
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X73112; CAA51538.1; EMBL; L20693; AAB05979.1; EMBL; L203095; CAA80641.1; EMBL; L20694; AAB02044.1; EMBL; L20694; CAA80640.1; EMBL; Z33094; CAA80640.1; EMBL; Z33481; CAA83889.1; EMBL; Z3481; CAA83889.1; EMBL; U66917; AAK50289.1;
                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-PSeudomonas sp. (strain ADP); STRAIN-ADP; PLASMID-PADB
Martinez B.M., Tomkins J., Wackett L.P., Wing R., Sadowsky M.:
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q934S8 PRELIMINARY; PRT; 151 AA.
Q934S8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                          Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS
                                                                                                                                                   PROSITE; PS00552; HTH_MERR_FAMILY; UNKNOWN_1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16555 MW; 26DDF7A510B082
                                                                                                                                                                                                                                                                                                                                                                                                             Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mer operon regulatory protein.
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                                                                                                                                                                                                                         REGULATORS.
EMBL; AJ251743; CAC69248.1; -.
                                                                                                                                                                                                                                                                    Russ.
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                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                            MERR
                                                                                                                                                                                              Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                      russ. J. Genet. 37:972-975(2001).
-!- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                ferrooxidans.";
                                                                                                                                                                                                                                                                                              "Tn5037, a Tn21-like mercury resistance transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 LVCACHARKGNVSCPLIASLQG 134
                                                                                                                                                                                                            InterPro; IPR000551; HTH_MerR.
                                          113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 LVCACHARKGNVSCPLIASLQG
                                                                    35 LVCACHARKGNVSCPLIASLQ 55
                                                                                                              Local
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                                         LVCACHARKGNVSCPLIASLQ 133
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                                                                                                              Similarity
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                                                                                                 Conservative
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100.0%; Pr
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                                                                                                              17.9%; Score 21; DB 2; 100.0%; Pred. No. 2.6e-1
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Pred. No.
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                                                                                                                                                      26DDF7A510B0829B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 subdivision; Acidithiobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                    Mismatches
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                                                                                                                2.6e-14;
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                                                                                                                                                                                                                                                                                                   from Thiobacillus
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RESULT 14
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Best Local (
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          SEQUENCE FROM N.A.
SPECIIS-A. Lwoffil; PLASMID-PKLH103, PKLH102, AND PKLH104; Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.
                                                                                                                                                                                                                                    SPECIES=A.calcoaceticus; PLASMID=PKLH2; MEDLINE=94134837; PubMed=8302940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acinetobacter sp.
Plasmid pKLH2, Plasmid pKLH103, Plasmid pKLH102, Plasmid pKLH104,
                                                                                                                   Plasmid 30:303-308(1993).
                                                                                                                                          "Molecular characterization of an aberrant mercury resistance transposable element from an environmental Acinetobacter stra
                                                                                                                                                                                       Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin Yurieva O.V., Nikiforov V.G.;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Lomovskaya O.L., Nikiforov V.G.;
Genetika 24:1064-1071(1988).
                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=A.calcoaceticus; PLASMID=PKLH2;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter calcoaceticus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mer operon regulatory protein.
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SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription x = 548460FCE50240FC CRC64;

SEQUENCE 151 AA; 16591 MW; 548460FCE50240FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bactería; Proteobactería;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens
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1; Z33487; CAA83895.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro; IPR000551; PF00376; merR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; gamma subdivision; Moraxellaceae;
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Nikiforov V.G.;
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100.0%; Pr
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01, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20;
Pred. No.
                                                                                                                                     environmental Acinetobacter strain.";
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               Z.M.,
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RESULT 15
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Q935L5;
01-DEC-2001 (TrEMBLrel. 19, C:
01-DEC-2001 (TrEMBLrel. 19, L:
01-MAR-2002 (TrEMBLrel. 20, L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF213017; AAA19678.1; -.
EMBL; AJ251539; CAB65953.1; -.
EMBL; AJ251517; CAB65939.1; -.
EMBL; AJ251009; CAB65945.1; -.
EMBL; AJ251009; CAB65949.1; -.
EMBL; AJ251706; CAC39408.1; -.
EMBL; AJ251706; CAC39408.1; -.
InterPro; IPR000551; HTH_MerR.
Pfan; PP00376; merR; 1.
Pfam; PF00376; merr; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; UNKNOWN_1.
DNA-binding; Plasmid; Transcription regulation;
SEQUENCE 151 AA; 16589 MW; 239344ADA01754AD
                                                                                                                                                                                                          Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
                                                                                    EMBL; AL513383; CAD09746.1;
                                                                                                                                                  "Complete genome sequence of a enterica serovar Typhi CT18.";
                                                                                                                                                                                                 Quail M., Rutherford K., Simmonds M., Skelton
                                                                                                                                                                                                                                                                                                                                 STRAIN-CT18
                                                                   InterPro; IPR000551; HTH_MerR.
                                                                                                                                     Nature 413:848-852(2001)
                                                                                                                                                                                     Whitehead
                                                                                                                                                                                                                                                                                                            MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pHCM1
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SMART; SM00422; HTH_MERR; 1.
SMOSTIE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; Transcription regulation.
SEQUENCE 151 AA; 16561 MW; 549350FCE50240FC CRC64;
                                                                                                                     -1 - SIMILARITY: BELONGS TO THE MERR
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The shuffling function of resolvases."; Gene 269:121-130(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=Acinetobacter sp.; STRAIN=ED45-25; PLASMID=PKLH205; MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "pKLH1-like aberrant mercury resistance transposons of environmental Acinetobacter strains: spread, polymorphism and possible origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDEC-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Enterobacteriaceae;
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Pred. No.
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. 2.9e-13;
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                                                                                                                   TRANSCRIPTIONAL
                                                                                                                                                                                             J., Stevens K.,
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        CRC64;
                  Complete proteome.
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Query Match 17.1%; Score 20; DB 16; Length 151; Best Local Similarity 100.0%; Pred. No. 2.9e-13; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: May 28, 2003, 10:41:38 Job time: 85 secs

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                  Issued_Patents_AA:*

1: /cgn2-6/ptodata/1/
2: /cgn2-6/ptodata/1/
3: /cgn2-6/ptodata/1/
4: /cgn2-6/ptodata/1/
5: /cgn2-6/ptodata/1/
6: /cgn2-6/ptodata/1/
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117
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                                                                                             /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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#### SUMMARIES

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US-09-362-871-2 US-08-164-292B-26 US-08-815-927-26 US-08-815-927-26 US-09-103-330-26 US-09-435-242-26 US-09-9435-242-26 US-09-958-489-36 US-09-058-489-36 US-09-058-489-36 US-09-058-489-36 US-09-181-148-22 US-09-182-950-9 US-09-182-736B-10 US-09-182-736B-10 US-09-183-736B-10 US-09-817-413-25 US-09-817-413-25 US-09-817-338-26 US-09-90-33-7388-10 US-09-063-7338-26 US-09-063-7338-26 US-09-063-7338-26 US-09-063-7338-26
sequence 2, Appli sequence 26, Appl sequence 26, Appl sequence 26, Appl sequence 26, Appl sequence 26, Appli sequence 26, Appli sequence 36, Appl sequence 35, Appl sequence 36, Appl sequence 22, Appl sequence 9, Appli sequence 10, Appl sequence 10, Appl sequence 25, Appl sequence 25, Appl sequence 25, Appl sequence 26, Appl

## ALIGNMENTS

US-08-948-097-2 RESULT 1

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APPLICANT: Skerra, Arne
APPLICANT: Voss, Selma
APPLICANT: Voss, Selma
TITLE OF INVENTION: Streptavidin Muteins
FILE REFERENCE: HUBR 1119
CURRENT APPLICATION NUMBER: US/08/948,097C
CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: DE 196 41 876.3
EARLIER FILING DATE: 1996-10-10
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08948097C ; patent No. 6103493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; GENERAL INFORMATION:
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Rothschil
APPLICANT: Gite, Sac
APPLICANT: Olejnik,
APPLICANT: UNENTION:
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                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09382950 Patent No. 6303337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                           SOFTWARE:
                                                                            CURRENT APPLICATION NUMBER: US/09/382,950
CURRENT FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Binding ligand for streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 8
TYPE: PRT ORGANISM: Artificial/Unknown
                                       LENGTH: 8
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                                                                                                                                                                    Gite, Sadanand
Olejnik, Jerzy
Olejnik, Jerzy
WENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
EMCE: AMBER-03879
                                                                                                                                                                                                                                                Rothschild, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Query Match
Best Local Similarity
""" hes 8; Conserve
                                                                            ; OTHER INFORMATION: designed sequence to act as an identifying tag US-09-619-103-9
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US-09-619-103-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-382-736B-8
                                                                                                                                                                              SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kurz, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-382-736B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/619,103
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09619103
Patent No. 6429300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic US-09-382-950-7
                                                                                                                                                                                                                                                                       APPLICANT: Kurz, Markus
APPLICANT: Lohse, Peter
APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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LENGTH: 8
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Patent No. 6306628
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rothschild, Kenneth
APPLICANT: Gite, Sadanand
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Prot
FILE REFERENCE: AMBER-03951
CURRENT APPLICATION NUMBER: US/09/382,736B
CURRENT FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
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Local Similarity 100.0%; Pred. No. 2e.
8; Conservative 0; Mismatches
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                                                                                                                                                                                   FastSEQ for Windows Version 4.0
                        Conservative
              6.0°; Pr.
                                6.8%; Score 8;
100.0%; Pred. No.
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                     Mismatches
                                           DB 4; Length 8;
2e+05;
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Thes 0; Indels
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           0; Gaps
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Sequence 105, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                   US-09-303-323-105
                                                                                                                                                                                                                                                                     RESULT 6
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Best Local Similarity 100.0%; Pred. No. ...
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPT
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-100-414B-105
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ZIP: 10134 VV. COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                          STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-JUNE-1:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. LIA
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                    CITY: New York
                                                                                                     STREET:
                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                              13 RMETVL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                               Morgan & Finnegan, L.L.P.
5 Park Avenue
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o. 11;
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OPERATING SYSTEM:

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US-09-100-414B-106
; Sequence 106, Application US/09100414B
; Patent No. 6025468
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; MOLECULE TYPE: peptide
US-09-303-323-105
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;Patent No. 5198345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 20-DEC-1985
SEQ ID NO:12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GWYNNE, DAVID I.; BUXTON, FRANCIS P.; PICKETT, MARK H.; DAVIES, ROGER W.; SCAZZOCCHIO, CLAUDIO
TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNGI
NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.1%; Score 6; DB 4; Best Local Similarity 100.0%; Pred. No. 11; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 105:
                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                      APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/10
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                             STREET: 345 Par
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                  COUNTRY:
                                                STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                          90 LSELVC 95
ZIP: 10154-0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 25
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                                                                                                                                                                                                                                                                                                                        9 LSELVC 14
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                                                                                                                                                                                                                                                                                                                                                                                        5.1%; Score 6; DB ilarity 100.0%; Pred. No. 14 Conservative 0; Mismatches
                  USA
                                                                                      Morgan & Finnegan, L.L.P.
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-106
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US-09-303-323-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: MOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 106, Application US/09303323 Patent No. 6228987
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Matches 6; Conserv
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                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106:
                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 212-758-4800
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MAILA H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11:
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compated operating system: PC will software: Word 97 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                     TELEPHONE: 212.751-6849
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/303,323 FILING DATE: 30-APR-1999
                                                                                                                                                                                                              FILING DATE: 20-JUNE-1998
                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 RMETVL 90
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 RMETVL 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,323
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                                 ENGTH:
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                  amino acid
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                                  31 amino acids
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IBM PC compatible
SYSTEM: PC Windows
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100.0%; Pred. No. 17;
tive 0; Mismatches
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APPLICATION NUMBER:

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; MOLECULE TYPE: US-09-303-323-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-468-853-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08468853 Patent No. 5670362
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LENGTH: 61
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: van de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5674
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APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 06-JUN-19
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 6; Conserv
                APPLICATION NUMBER: US 08/310,357 FILING DATE: 21-SEP-1994
                                                                                                                                                                                                                                                             COUNTRY: UZIP: 20850
                                                                                                                                                                                                                                                                                                STATE: Maryland
                                                                                                                                                                                                                                                                                                                       CITY: Rockville
                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 PLIASL 55
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                                                                                               06-JUN-1995
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100.0%; Pred. No. 32)
tive 0; Mismatches
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5. 17;
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US-08-468-855-4
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TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATY E. GOTTHLEY
REGISTRATION NUMBER: 34,40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
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                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 08/102,865
APPLICATION NUMBER: US 08/102,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5780289el Patent Department
STREET: 1300 Piccard Drive
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1992
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NAME: Mary E. Gormley REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                  FILING DATE:
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CITY: Rockville
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GY: linear
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06-AUG-1993
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100.0%; Pr
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0; Mismatches
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5. 65;
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RESULT 13
US-08-310-357-4
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Matches 6
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                                                                                                   Query Match
                                                                   Matches
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                                                                                                                                                                                                                                            TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
NAME: William M. Blackstone
REGISTRATION NUMBER: 29,772
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Rockville
STATE: Maryland
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Local Similarity 100.0%; Pred. No. 65
hes 6; Conservative 0; Mismatches
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                                                                   Local Similarity
les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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 41
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 EEASSL 46
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                                                                   Conservative
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                                                                 5.1%; Score 6; DB:
100.0%; Pred. No. 65
tive 0; Mismatches
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US-08-468-852-4
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US-08-468-857-4
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                                                                                                                                          Sequence 4, Application US/08468857 Patent No. 5925347
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                                                                                                                                                                                                                                                                                                                                                                                 Best
                 GENERAL INFORMATION:
APPLICANT: Van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERWEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATY E. GOTTMLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: van den BOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERWEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,409
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0: FILING DATE: 06-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                           y Match 5.1%; Score 6; DB Local Similarity 100.0%; Pred. No. 65 nes 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                           41 EEASSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                 5 EEASSL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 amino acids
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ADDRESSEE: Akzo No. 592347el Patent Department
CITY: Rockville
STRET: 1300 Piccard Drive
STRET: 1300 Piccard Drive
STRET: Maryland
COUNTRY: U.S.A.
ZIP: JO850 A.
ZIP: JO85
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0;

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Total number of hits satisfying chosen parameters:
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DB seq length: 2000000000
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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1. /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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203.565 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

Query

#### ALIGNMENTS

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RESULT 2
US-10-104-218-5
                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517a-6
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US-09-809-517A-6
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Patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/pr
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
Sequence 5, Application US/10104218
Patent No. US20020177196A1
GENERAL INFORMATION:
APPLICANT: MAIER, Thomas
APPLICANT: MAEBERT, Carsten
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PROTEINOGENIC L-AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 10
TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                        108 SAWSHPQFEK 117
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100.0%; Pred. No. 0.00075;
... Mismatches 0;
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US-10-001-934-8
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                                                                                             Sequence 8, Application US/10001934 Publication No. US20030032782A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 9
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                 APPLICANT: NAGY, ZOLTAN
TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
FILE REFERENCE: GPCG-P01-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT ETLING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
 CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/104,218
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: German No. US20020177196A1 101 16 881.0
PRIOR FILING DATE: 2001-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kurz, Markus
APPLICANT: Lohse, Pete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: MAIER, T. ET AL.-2
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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les 8; Conserv
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mes 8; Conserv
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US/10/001,934
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NO. 3.4e+05;
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US-10-026-578B-9
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US-10-001-934-8
                                                                                                                                                                                                                                                              RESULT 6
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Best Local Similarity
Thes 8; Conservi
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                                                                                                                                                                                                     Sequence 9, Application US/10026578B Publication No. US20030083474A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 8
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
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Best Local Similarity
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APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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              CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11 PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21
                                                                            APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
FILE REFERENCE: 100810.01US1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
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100.0%; Pr
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100.0%;
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o. 3.4e+05;
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RESULT 7
US-10-174-368A-7
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US-09-809-517A-9
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                                     Sequence 9, Application US/09809517A
Patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10174368A Publication No. US20030092031A1 GENERAL INFORMATION:
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SEQ ID NO 7
LENCTH: 8
TYPE: PRT
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APPLICANT: Gite, Sadanand
APPLICANT: Gite, Sadanand
APPLICANT: Olipink, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Profile Reference: AMBER-07145
CURRENT APPLICATION NUMBER: US/10/174,368A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/049,332
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/382,736
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
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                      CURRENT APPLICATION NUMBER: US/09/809,517
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ORGANISM: Artificial Sequence
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  2001-03-15
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lo. 3.4e+05;
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-9
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Best Local Similarity
Best Local Similarity
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US-09-983-067-3
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SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 7
LENGTH: 8
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 8
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Best Local (
APPLICANT: INOUE, Akio
APPLICANT: SHIMIZU, Yoshihiro
APPLICANT: UEDA, Takuya
APPLICANT: UEDA, Takuya
TITLE OF INVENTION: Process for Producing Peptides By Using In Vitro
TITLE OF INVENTION: Transcription/Translation System
FILE REFERENCE: 1752-0151P
CURRENT APPLICATION NUMBER: US/09/983,067
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rothschild, Kenneth J.
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in
FILE REFERENCE: AMBER-06819
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CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/382,950
PRIOR FILING DATE: 1999-08-25
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100.0%; Pr
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100.0%; Pred. No. 3.
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No. 3.4e+05;
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PRIOR APPLICATION NUMBER: JP 294795/200:

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US-09-809-517A-33
Sequence 33, Application US/09809517A
Patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US2002003473:
TITLE OF INVENTION: particles via d.
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Best Local Similarity
Triphes 8; Conserv
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PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 21
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GENERAL INFORMATION:
APPLICANT: Lohning, Corin
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Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
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PRIOR APPLICATION NUMBER: JP 6910/2001
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 401417/2000
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
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Corinna No. US20020034733Alel methods for displaying (poly)peptides/prote particles via disulfide bonds
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Pred. No.
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US-10-026-578B-3
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LENGTH: 24
TYPE: PRT
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LENGTH: 22
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CURRENT FILING DATE: 2002-11-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
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LOCATION: (9)..(9)
OTHER INFORMATION: X represents a single amino acid at the position indicated
                                                                                        OTHER INFORMATION: X represents a single amino acid at the position indicated
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OTHER INFORMATION: X represents a single
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OTHER INFORMATION: X represents
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                                                NAME/KEY: MISC_FEATURE
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mes 8; Conserv
ION: (14)..(14)
INFORMATION: X represents a single amino acid at the position indicated
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RESULT 14
US-10-026-578B-4
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TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 24
TYPE: PRT
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APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
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Best Local
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                                                                                                                               NAME/KEY: MISC_FEATURE LOCATION: (13)..(13) OTHER INFORMATION: X represents
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OTHER INFORMATION: X represents
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LOCATION: (9)..(9)
OTHER_INFORMATION: X represents a single
                                                             LOCATION: (14)..(14)
OTHER INFORMATION: X represents
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OTHER INFORMATION: X represents
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NAME/KEY: MISC_FEATURE
LOCATION: (11)..(11)
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LOCATION: (10)...(10)
OTHER INFORMATION: X represents a single
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 LOCATION: (15)..(15)
OTHER INFORMATION: X
                                                                                               NAME/KEY: MISC_FEATURE
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                                 NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: Artificial Sequence represents peptide
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OTHER INFORMATION: X represents a
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OTHER INFORMATION: X represents a single amino acid at the position indicated
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                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 31 LENGTH: 24 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/09809517A
patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: LOhning, Corinna
TITLE OF INVENTION: No. US20020034733A1e1 methods for displaying (poly)peptides/pr
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
                                                                    Best Local Similarity Matches 8; Conser
                                                                                                     Query Match
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Best Local
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                                                                                                                                                      OTHER INFORMATION: Description
                                                                                                                                                                                     ORGANISM: artificial sequence
                                                                                                                                                                            FEATURE:
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OTHER INFORMATION: X represents a
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LOCATION: (22)..(22)
OTHER INFORMATION: X represents
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OTHER INFORMATION: X represents a
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OTHER INFORMATION: X represents a single amino
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17 WSHPQFEK
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                                                                                   Score 8; DB 10;
Pred. No. 0.2;
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Search completed: May 28,

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Job time : 58 secs

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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117
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                    /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
/cgn2_6/ptodata/1/paa/US092_COMB.pep:*
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227.210 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

6	5	4	w	2	1	Result No.
57	57	57	57	64	117	Score
48.7	48.7	48.7	48.7	54.7	100.0	Query Match
117	117	117	117	117	117	Query Match Length DB ID
23	23	23	23	23	23	DB
US-09-977-137A-9	US-09-977-137A-8	US-09-977-137A-7	US-09-977-137A-5	US-09-977-137A-12	US-09-977-137A-4	Length DB ID
Sequence 9, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 12, Appl	Sequence 4, Appli	Description

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1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60

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US-09-764-854-359	-09-620-394B-3	-09-513-996A-15	-60-360-039-2022	S-60-312-544-100	-10-219-999-6154	-09-980-862-	-09-980-862-2	15-127-1	9-980-862-	9-980-862-2	-980-862-2	-09-980-862-2	-09-979-284-1	-09-809-517A-3	-09-809-517A-	-09-809-517A-3	-09-809-517A-3	-09-983-067-	8-357-	1	-10-049-332-	-10-001-934-	-09-973-145-	-09-809-517A-	-09-809-517A-	S-09-252-991A-2525	-09-252-991A-23	-09-252-991A-2515	-09-977-137A-	-09-252-69	S-09-252-691-6	9-039A-	US-09-252-691C-5823	52-691-5	77-137A-	-09-977-137A-1	US-09-977-137A-10	
Sequence 359, App	Sequence 3514	Φ	e 20227	e 1006	6154	e 27,	e 26, A	e 1007	Sequence 19, Appl	e 22,	equence 20,	24,	19,	e 34,	Φ	33,	30,	10	e 9,	ю 57	e 8,	e 8, Appl	e 7,	9	e 6,	e 25251,	e 23125,	e 25151,	equence 6, App	e 60	equence 6093,	e 11501,	e 5823,	e 582	e 2,	Sequence 11, Appl	Ó	

### ALIGNMENTS

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RESULF 1
US-09-977-137A-4
; Sequence 4, Application US/09977137A
; Sequence 4, Application US/09977137A
; GENERAL INFORMATION; Mortal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION; Metal Binding Proteins, Recombinant Host Cells and FILE REFERENCE: 79-00
; TITLE OF INVENTION; Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION; Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION; Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION; Metal Binding Proteins, Recombinant Host Cells and TITLE REFERENCE: 79-00
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRI ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-4

Query Match 100.0%; Score 117; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.3e-113;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps
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MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60

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                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09977137A
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09977137A
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
                                                                                                  Query Match
                                                                                                                                                                                                                                     SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 79-00
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ORGANISM: Artificial Sequence
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                                                                                                                                                                    FEATURE:
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SSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEE 64
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                                                                Score 57; DB; Pred. No. 9.8
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; Pred. No.
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                                                                              DB 23; 1
9.8e-51;
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US-09-977-137A-7
                                                                                              US-09-977-137A-9
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                                                                                                                  RESULT 6
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 117
                                                        Sequence 9, Application US/09977137A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 117
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Best Local :
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Metal Binding Proteins, TITLE OF INVENTION: Methods FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
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les 57; Conserva
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Pred. No.
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. 9.8e-51;
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hes 0;
    Recombinant Host Cells and
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TITLE OF INVENTION:

Methods

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US-09-977-137A-11
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 10
LENCTH: 117
TYPE: PRT
SEQ ID NO 11
                                                                                                                                                                                                                                           Sequence 11, Application US/09977137A GENERAL INFORMATION:
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Best Local Similarity
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                                                       PRIOR APPLICATION NUMBER: US 60/240,465 PRIOR FILING DATE: 2000-10-12
                                                                                           CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
                                                                                                                                     APPLICANT: Caguiat, Jonathan TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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              NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                     APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
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ORGANISM: Artificial Sequence
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nes 57; Conserv
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Pred. No.
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9.8e-51;
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                                                                                                                                                                           SEQ ID NO 5823
LENGTH: 220
TYPE: PRT
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GENERAL INFORMATION:
                                                                        Matches
                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
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TYPE: PRT
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80 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
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                                                                       Conservative
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100.0%;
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100.0%; Pred. No
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Pred. No.
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Pred. No. 1.4e-4
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                                                                                         No.
                                                                                     DB 16; 1, 2.1e-48;
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hes 0;
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PRIOR EPLING DATE: 1998-07-24;
PRIOR APPLICATION NUMBER: US 60/074,787;
PRIOR FILING DATE: 1998-02-18;
NUMBER OF SEQ ID NOS: 11326;
SEQ ID NO 5823;
LENGTH: 220;
TYPE: pom
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US-09-252-691-6093
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US-09-489-039A-11501
; Sequence 11501, Application US/09489039A
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                 CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 6093
LENGTH: 255
TYPE: PRT
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                            Sequence 6093, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND
ENTRE DEFENSE: 107106 115
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PRIOR FILING DATE: 1999-01-29
RUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11501
LENGTH: 221
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Best Local
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                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/489,039A
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
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ORGANISM: Enterobacter cloacae
ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                           157 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 211
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les 55; Conserv
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2.1e-48;
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US-09-252-691-6093
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SEQ ID NO 6093
LENGTH: 255
TYPE: PRT
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APPLICANT: Keith G
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,691C CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,787 PRIOR FILING DATE: 1998-02-18
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Sequence 6, Application US/09977137A

GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Methal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: chelon
US-09-977-137A-6
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US-09-977-137A-6
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Search completed: May 28, 2003, 10:48:43 Job time: 332 secs
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                                                                                                                                               Ouery Match 41.0%; Score 48; DB 23; Length 118; Best Local Similarity 100.0%; Pred. No. 2.3e-41; Matches 48; Conservative 0; Mismatches 0; Indels
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US-09-232-279-1
US-08-08-2847-1
US-09-035-558-1
US-09-007-005-17
US-09-244-796-17
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US-08-676-974-5
US-08-676-974-5
US-08-676-974-5
US-08-676-974-5
US-08-199-637A-160
US-09-199-637A-114
US-09-199-637A-114
US-09-199-637A-114
US-09-199-637A-114
US-09-103-840A-1
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US-09-889-595-4
US-08-818-112-12
US-08-818-111-12
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Sequence 1, Appli
Sequence 1, Appli
Sequence 17, Appl
Sequence 17, Appli
Sequence 2, Appli
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Sequence 3, Appli
Sequence 3, Appli
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Sequence 6, Appli
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Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 13, App
Sequence 114, App
Sequence 114, App
Sequence 79, Appli
Sequence 79, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence
Sequence
Sequence
4, Appli
12, Appl
12, Appl
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RESULT 2 US-08-682-847-1

Sequence 1, Application US/08682847
Patent No. 5858989
GENERAL INFORMATION:

APPLICANT: BABIUK, LORNE
APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: FITZPATRICK, DAVID

ZAMB, TIM
FITZPATRICK, DAVID

TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1

ОУ ОУ ОУ ОУ	D Qy	US U	o
	Query M Best Lo Matches	RESULT 1 US-09-232-279 Sequence 1, Patent NO. GENERAL INF APPLICANT: TITLE OF I TITLE OF I TITLE CURRENT AP CURRENT AP CURRENT AP CURRENT OF SOFTWARE: SEQ ID NO ILENGTH: 2 TYPE: DNA ORGANISM: US-09-232-279	22888888888888888888888888888888888888
69 CG   1971 GG   129 GG   2031 GG   189 GG   189 GG	atch cal s 107 9	1 232-279-1 ence 1, Applicatence 1, Application 2, Applicat	30.66 30.66 30.44 30.44 30.44 30.44 30.44 30.44 30.44 30.44 30.44 30.44 30.44 30.44 30.46
ACTTGGCGC	11. Similarity 47. 7; Conservative CTGCGAGGAGGCCAG	ratic 73 73 coneet coneet ION: 10N: 1454: TION 84: DATE: DATE: DNOS ntIn 1	
GCCCATO	11.: 47.: 47.: 7ative 3GCCAGO 1 11 CGAGAGO	tion US/0923 : et et al. :: POLYNUCLE :: POL	1155 1155 4171 4171 5058 15058 15058 1027 23673 3760 3760 3760 3760 2505 2505 2505 2713 3472 11236
GGC CCC	3%; 6%; 6%; 1 3CGA	0923: 0CLE 0CLE 1NG 1 50 : US: -01-:	444444444444444444444444444444444444444
CGACTTGGCGCCATGGAAACCGTGCTGTTGAACTCGTGTGCGCGTGCCATGCACGAAA	11.3%; Score 36.2; DB 4; Length 2799; imilarity 47.6%; Pred. No. 0.28; Conservative 0; Mismatches 118; Indels 0; Gaps CTGCGAGGAGCCAGCCTGGCCGAACAAGCTCAAGGACGTGCGCGAGAAGATGGC	2279  OTIDE VACCINE FORMULA, BOVINE RESPIRATORY DISE 8/09/232,279 15	US-09-056-556-12 US-09-072-596-12 US-09-754-250-1 US-09-889-595-1 US-08-807-044-2 US-08-680-326-23 US-08-724-354D-1 US-09-773-816-1 US-09-770-984A-1 US-09-777-434-7 US-08-748-819-7 PCT-US91-07035-7 US-08-458-819-7 PCT-US91-07035-7 US-08-804-439A-13 US-08-720-229-13 US-07-853-913-1
SGCTGCCATGCACGAAA 128	Length 2799; Indels 0; Gaps 0; GACGTGCGCGAGAAGATGGC 68	PARTICULARLY FOR	Sequence 12, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 13, Appli

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER

ADDRESSEE: MURALUL ROAD STREET: 755 PAGE MILL ROAD

STREET: 755 PAG CITY: PALO ALTO

TITLE OF INVENTION: NUMBER OF SEQUENCES:

POLYPEPTIDES AND VACCINES

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us-08-035-558-1
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; LOCATION:
US-08-682-847-1
                                                                                                                                                                            Sequence 1, Application US/08035558 Patent No. 5462734 GENERAL INFORMATION:
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 2931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                  APPLICANT: Letchworth, Geoffr
APPLICANT: Israel, Barbara A.
TITLE OF INVENTION: HERPESVIR
TITLE OF INVENTION: OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LENGTH: 3382 base pair
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                                      ADDRESSEE:
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 12-JUL-1996
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EDNESS: double
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FIRST WISCONSIN PLAZA
                    E: Quarles and Brady P.O BOX 2113
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                                                                             HERPESVIRUS VACCINE AND METHOD OF USING SAME
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Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118;
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RESULT 4

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Best Local Similarity 47.6%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (608)251-9166
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: r
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (608)251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Nelson, Randy
AUTHORS: Smith, Michael
TITLE: Sequence of a Bovine Herpesvirus Type-1 etc.
JOURNAL: Virology
VOLUME: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: coding sequence for gI glycoprotein LOCATION: 379 to 3165
IDENTIFICATION METHOD: sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: bovine herpervirus-1 INDIVIDUAL ISOLATE: P8-2 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/6
FILING DATE: 02-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Nicholas J. S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
    2460
                                                                                                                                                           2340 GGGCCGCGAGCTCGTGGAGCCCTGCACCGCCAACCACAAGCGCTACTTCCGCTTTGGCGC 2399
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                                                                                                                                                                                                  69 CGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAA 128
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                        GGAGGCCAGCCTGGCCGAACACACAGGTCAAGGACGTGCGCGA 233
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GGTGATCAGCACCTTTGTGGACCTAAACCTCACGGTTCTGGAGGA 2504
                                                                            GGACTACGTGTACTACGAGAACTACGCGTACGTGCGGCGGGTCCCGCTCGCGGAGCTGGA
                                                                                                                   GGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGA 188
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         1: FROM 379 TO
                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                           Length 3519;
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us-09-007-005-17

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CURRENT APPLICATION NUMBER: US/09/007,005B;
CURRENT FILING DATE: 1998-01-14
EEARLIER APPLICATION UNMBER: 60/035,963
EEARLIER FILING DATE: 1997-01-27
EEARLIER APPLICATION UNMBER: 60/064,491
EEARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09244796 Patent No. 6281344
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                    TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007

CURRENT APPLICATION NUMBER: US/09/244,796

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/035,963

EARLIER FILING DATE: 1997-01-27

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER FILING DATE: 1997-11-06

EARLIER FILING DATE: 1998-01-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Artificial Sequence
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Pred. No. 0.3;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C
US-09-244-796-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 4403765
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APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAITIFLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US,09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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791142 GCGCCCTGGTCGTCGGCGCATTCGGCGGACATATCGTCTGGCTGTCGGGACGGCTCGGCC
                                                                            791082 GCGCCCATCGCCGAAGTGTTAGACCAAACTCAGGCCTAGAGCTGACCTAGGTGGCAGCGG 791141
                                     136 GTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCC 195
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Pred. No. 4.1;
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
           ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: Edward H. Gorman
                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                   STREET: Abbott 1
STREET: Park Rd
CITY: Abbott Par
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                               COUNTRY:
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                                                                                                                                   Abbott Park
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PC-DOS/MS-DOS
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27
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Pred. No. 4.1;
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NFORMATION FOR SEQ ID NO:
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LOCATION: 19..10722
OTHER INFORMATION: /c
OTHER INFORMATION: /f
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OTHER INFORMATION: 6
                   FEATURE:
                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                FEATURE:
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NAME: Danckers, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LENGTH: 20235 base pai
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LOCATION:
                                     OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module
                                                                      NAME/KEY: misc_feature
LOCATION: 6054..7026
                                                                                                                               OTHER INFORMATION: /function- "approximate OTHER INFORMATION: beta-ketoacylACPsynhase
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LOCATION:
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OTHER INFORMATION: /fur OTHER INFORMATION: beta
 NAME/KEY:
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REGISTRATION NUMBER: 3265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: NRRL 238
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4171..4428
misc_feature
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acyltransferase domain of module 4"
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module 3"
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module 4"
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/function= "gene eryA"
/product= "eryA oRF2 encoding modules 3 & 4 for
6-deoxyerythronolide B"
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NAME/KEY: misc_feat
LOCATION: 14062..14
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NAME/KEY:
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OTHER INFORMATION:
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LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
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OTHER INFORMATION: 6-deoxyerythronolide B formatio"
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                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 40,943
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Best Local S
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APPLICANT: Mcalpine, JB
TITLE OF INVENTION: Method of Directing Biosynthesis
TITLE OF INVENTION: Specific Polyketides
TITLE OF GROUENCES: 27
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                 MOLECULE TYPE: DN
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                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                    HYPOTHETICAL:
ANTI-SENSE: NO
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STREET:
CITY: Ab
                              ORGANISM: Saccharopolyspora erythraea STRAIN: NRRL 238
                                                                                                                                   STRANDEDNESS: doul TOPOLOGY: unknown
NAME/KEY:
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Abbott Laboratories D377/AP6D-2 One Abbott
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LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4
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OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain module 3
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LOCATION: 4471..5847
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LOCATION: 4471..10722
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LOCATION: 4171..4428
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acyltransferase
/function=
module 5"
    module
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                                                                                           /function= "gene =eryA"
/product= "orf3 encoding modules 5
6-deoxyerythronolide B formatio"
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module 4"
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module 3"
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beta-ketoacyl ACP synthase of module
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                    "approximate span
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LOCATION: 14062.14610
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
FEATURE:
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OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feat
LOCATION: 12379..13
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NAME/KEY: misc_feature

15172..16569
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LOCATION: 15166..20235
OTHER INFORMATION: /fun
OTHER INFORMATION: modu
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LOCATION: 19149..1939
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
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LOCATION: 18379..18921
OTHER INFORMATION: /fun
OTHER INFORMATION: beta
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3831 C
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Similarity 53.0%;
                                                                   misc_feature
12379..13350
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14857..15114
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acyltransferase domain of module
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thioesterase domain of module 6"
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beta-ketoreductase domain of module
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beta-ketoacylACPsynthase domain of modul"
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beta-ketoacylACPsynthase domain of modul"
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beta-ketoreductase of module
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module 6"
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Pred. No. 1.9;
0; Mismatches 82;
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RESULT 10

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us-08-676-967-5

Application US/08676967

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US-08-676-974-5
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Best Local :
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                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08676974 Patent No. 5770422
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APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
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TELEPHONE: (415)343-4341
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MEDIUM TYPE: Floppy disk
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NAME: Osman Ph.D., Richard A
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CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
                                                                                                          COUNTRY:
ZIP: 941
           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CITY: San Francisco
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CITY: San Francisco
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                                                                                                                                                STATE:
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Pred. No. 1.8;
0; Mismatches
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; MOLECULE TYPE: US-09-098-487-5
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US-08-676-974-5
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Query Match
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                                                                                                                                                             TELEFAX: (415)343-4342 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COLLINS, KALILLEL.
APPLICANT: COLLINS, Human Telomerase
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 11
CORRESPEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
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REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Osman Ph.D., Richard A
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415)343-4341
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NAME: OSMAN Ph.D., RICHART A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
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                                                                                     STRANDEDNESS:
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CLASSIFICATION:
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                                                                       TOPOLOGY:
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                                                                                                                         LENGTH:
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DEDNESS: double
                                                                                     nucleic acid
EDNESS: double
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67.1%;
10.3%;
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                                                                                                                                                                                                                                     0СВ96-055
 Score 33.2;
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 DB 2;
Length 2277;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/246,489 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lan, Michael S.
APPLICANT: No. 6225049kins, Abner L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: doub
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ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/901,715
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                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                            864 CGTGCTGGGGCTCAAGATCAAGGAGGGCCCCGGTGGAGGCGCCGCGGGGGCCGCGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        842 GCGACCAGCGAGGAGGACAGCGACCTGGAGGAGCGACAGCATCGACGACGACGAGG 901
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                                                                                                                                                            120;
                                                                                                                               27
                                                  AACCGTGCTGTCTGAACTCGTGTGCGCCCTGCCATGCACGAAAGGGGAATGTTTCCTGCCC 146
                              CGCGGCGCGGCCGCTGGGCGAGTTCATCTGCCAGCTGTGCAAGGAGGAGTACGCCGACCC
GTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCCAGCAGCCTGGC
                                                                                                                          CCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 86
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Pred. No.
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SEQ ID NO 160
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-160
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US-08-173-508-5
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                                                                                                                                                                                        Sequence 5, Application US/08173508 Patent No. 5616485
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Best Local
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APPLICANT:
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bartfe
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CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
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PRIOR FILING DATE: 1997-11-25
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                CORRESPONDENCE ADDRESS:
                             NUMBER OF SEQUENCES:
ADDRESSEE:
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Mahajan-Miklos, Shalina
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Foley & Lardner
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APPLICANT: TSONGALIS, JOHN
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION
TITLE OF INVENTION: POLYPEPTIDES
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Pred. No. 2.1;
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                                    STRAINS FOR EXPRESSION OF PEPTIDES AND
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ZIP: 2007-5109
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NOMBER: US/08/173,508
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 18740/125/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5309
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 190..192
; OTHER INFORMATION: /note= "Met at position 1
; OTHER INFORMATION: represents fmet"
US-08-173-508-5
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Search completed: June Job time : 57 secs
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NAME/KEY:
LOCATION:
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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seq length: 20
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-044-090-167
US-10-014-090-167
US-10-175-523-48
US-09-954-456-966
US-09-954-456-1143
US-09-954-456-1143
US-09-759-130B-449
US-09-759-130B-449
US-10-021-955-72
US-10-021-955-72
US-10-021-955-73
US-10-021-955-75
US-09-975-719-160
US-09-975-719-160
US-09-815-242-4163
US-09-815-242-4281
US-10-040-739-249
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US-09-815-242-7812
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3182.538 Million cell updates/sec
                                                                                                                                                                     Sequence 17, Appl
Sequence 1, Appli
Sequence 167, App
Sequence 48, Appl
Sequence 700, App
Sequence 966, App
Sequence 1143, Ap
                                                                                                                                                                                                                                                                                                                                         Description
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7812, Ap
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30.6	30. 6	30.6	30.8	30.8	30.8	31	31	31	31	31	31	31	31.2	31.2	31.2	31.2				31.2			31.4	31.4
9.5	о ч	9.51	9.6	9.6	9.6	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.8	9.8
3999	2421	245	2826	1575	968	2839	2839	2293	2016	837	837	394	15872	15872	15872	15872	7419	2711	2051	1632	1341	222	88421	349
9 6	10	10	10	10	10	9	9	10	10	9	9	9	10	9	9	9	10	9	9	9	9	10	9	9
US-09-738-626-548	US-09-804-701-7033	US-09-864-761-23764	US-09-925-297-203	US-09-917-800A-1540	US-09-864-866-46	US-10-105-891-89	US-10-125-237-89	US-09-729-674-157	US-09-764-864-744	US-10-184-634-454	US-10-184-644-454	US-10-040-739-1151	US-09-861-289-1	US-09-836-821-1	US-09-988-384B-1	US-09-860-846-1	US-09-815-242-4009	US-09-772-180A-1	US-09-975-719-114	US-09-772-180A-7	US-09-975-719-133	US-09-294-093B-3769	US-09-976-059-1	US-10-040-862-4282
548,	Sequence 7677, Ap	Sequence 23/64, A		Sequence 1540, Ap	Sequence 46, Appl	Sequence 89, Appl	Sequence 89, Appl	Sequence 157, App	Sequence 744, App	Sequence 454, App	Sequence 454, App	Sequence 1151, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 4009, Ap	Sequence 1, Appli	Sequence 114, App	Sequence 7, Appli	Sequence 133, App	Sequence 3769, Ap	Sequence 1, Appli	Sequence 4282, Ap

## ALIGNMENTS

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US-10-085-519-1
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Patent No. US20020160018A1
GENERAL INFORMATION:
APPLICANT: AUGORET et al.
TITLE OF INVENTION: POLYNICLEOTIDE VACCINE FORMULA, PARTICULARLY FOR TITLE OF INVENTION: TREATING BOVINE RESPIRATORY DISEASE
FILE REFERENCE: 454313-2250
FULE REPERENCE: 454313-2250
CURRENT APPLICATION NUMBER: US/10/085,519
CURRENT EILING DATE: 2020-02-28
PRIOR APPLICATION NUMBER: 09/232,279
PRIOR FILING DATE: 1999-01-15
NUMBER: FILING DATE: 1999-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 1
LENGTH: 2799
                                                                                                                                                                                                                                                                                                                                                                                                                          uery Match 11.3%;
Best Local Similarity 47.6%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Bovine herpesvirus 2
2091 GGTGATCAGCACCTTTGTGGACCTAAACCTCACGGTTCTGGAGGA 2135
                                                                                                        2031 GGACTACGTGTACTACGAGAACTACGCGTACGTGCGGCGGGTCCCGGCTCGCGGAGCTGGA 2090
                                                                                                                                                                                                                     1971 GGGCCGCGAGCTCGTGGAGCCCTGCACCGCCAACCACAAGCGCTACTTCCGCTTTGGCGC
                                                                                                                                                                                                                                                                                                                             1911 CTTCGGCAACGAGAGCGAGCCGGTGGAGGGCCAGCTCGGCGAGGACAACGAGCTGCTGCC
                               189 GGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGA 233
                                                                                                                                                                                                                                                                      69 CGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                 9 CTGCGAGGAGGCCAGCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATGGC
                                                                                                                                                            GGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 118; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.2; DB 9; Length 2799; Pred. No. 0.029;
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Sequence 1, Appli Sequence 72, Appl Sequence 75, Appl Sequence 160, App Sequence 4163, Ap Sequence 4081, Ap Sequence 249, App

Sequence 79, Appl Sequence 449, App

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US-10-166-087-17

Sequence 17, Application US/10166087

Publication No. US20030077767A1

GENERAL INFORMATION:
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                                                                                                 RESULT 3
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; LOCATION: (1).
US-09-815-242-7812
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/223,625
PRIOR APPLICATION NUMBER: 60/253,625
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US-09-815-242-7812
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SEQ ID NO 7812
LENGTH: 1431
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                             1104
                                                                                                                                                                           1164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                       1044 GGGCGCGTCCATCGACAAGCAGGACCATGCCGCGAATCCGTGCGGCCAGATCGGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                            135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    924 GCCGTGAGCTGCGAGGCGAACCCGAAGCGCACCGCCGACATCCCGACCCTGGCGCAAAT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 GGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTT 74
                                                                                                                                                                      CCTGGTGATCGTCACCGCCGACCACGCCCACTCCAGCCA 1202
                                                                                                                                                                                                                  CATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCA 293
                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCAGCAAGGCCATCGAGCTGCTGAAGGACAATCCGAACGGCTTCTTCCTGCAGGTCGA 1043
                                                                                                                                                                                                                                                                        CGTCGACCTCGACGAAGCCGTGCAGAAGGCCCTTGGCCAAGGCCGATGGCGAGAC
                                                                                                                                                                                                                                                                                                                      CAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 0.036;
0; Mismatches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1431;
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US-10-044-090-167

Sequence 167, Application US/10044090

Patent No. US20020137081A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQ ID NO 1
; LENGTH: 32539
; TYPE: DNA
; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-1
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US-10-166-087-1
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                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 2295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3014-2US
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
FITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3014-2US
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ecopia Biosciences Inc
APPLICANT: Farnet, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces refuineus subspecies thermotolerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 10.8%;
Local Similarity 58.1%;
                                                                                                                                                           11419 GATCACCGAGCTGGGGCGCATCGACGACCCGGTGGCCGAACCCAT 11463
                                                                                                                                                                                                                                                   11359 CGCCTCCAGGATCGACGGCAAGAACATCGCCGACTACGCCGCCATGGAGGTGAGCGAACT 11418
                                                                                                                                                                                    237 GATGGCCGACTTGGCCGCGCGCATGGAACCCGTGCTGTCTGAACTCGT 281
                                                                                                                                                                                                                                                                                             177 CACCCACTGCGAGGAGGCCAGCCCTGGCCGAACACCAAGCTCAAGGACGTGCGCGAGAA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903 GATCACCGAGCTGGGGCGCATCGACGACCCGGTGGCCGAACCCAT 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           843 CGCCTCCAGGATCGACGGCAAGAACATCGCCGACTACGCCGCCATGGAGGTGAGCGAACT 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 CACCCACTGCGAGGAGGCCAGCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 GATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
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Staffa, Alfredo
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                           10.8%;
58.1%;
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                                                                                                                                                                                                                                                                                                                                         Score 34.6; DE Pred. No. 0.13; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Length 32539;
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT FILING DATE:

2002-01-09

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; ORGANISM: Homo sapiens US-10-175-523-48
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                 Query Match
                                                                                                   SEQ ID NO 48
LENGTH: 2838
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1J795-US3
CURRENT APPLICATION NUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-25
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                                                                                                                                                                       PRIOR FILING DATE:
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OTHER INFORMATION: Inc;
                                                                                   TYPE: DNA
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                                                                                                                                                                                  APPLICATION NUMBER: US 60/333,047
FILING DATE: 2001-11-14
APPLICATION NUMBER: US 60/349,936
FILING DATE: 2002-01-18
APPLICATION NUMBER: US 60/361,834
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No. US20030096264A1
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Rajan, Prithi
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SEQ ID NO 700
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                                                                                                                                                                                         Query Match 10.3%;
Best Local Similarity 45.3%;
                                                                                                                                                                       Matches
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CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
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PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
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PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
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PRIOR FILING DATE: 2000-09-27
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924 CGCGGCGCGGCCGGCCGAGTTCATCTGCCAGCTGTGCAAGGAGGAGTACGCCGACCC
                                                                                    864 CGTGCTGGGGCTCAAGATCAAGGAGGGCCCCGGTGGAGGCCGCGCGGGGGCCGCGCGGGGGGG
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                                        87 AACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATGTTTCCTGCCC 146
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                                                                                                                             27 CCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 86
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; ORGANISM: Homo sapiens
US-09-954-456-966
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US-09-954-456-966
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SEQ ID NO 966
TOUGHH: 2838
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Best Local
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NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
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CURRENT FILING DATE: 2001-09-18
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APPLICATION NUMBER: US/60/235,840
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APPLICATION NUMBER: US/60/235,720
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FILING DATE: 2000-09-26
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                        1044 GTGCGCCAAGGTCTTCAGCTGCCCGGCCAACCTGGCCTCGCACCGCCGCCGCTGGCACAAACC 1103
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                                                                                                                                                                                                                                          87 AACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGGAATGTTTCCTGCCC 146
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                                                                   CGAACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAACCGT 266
                                                                                                             GTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCCAGCAGCCTGGC 206
                                                                                                                                                                                                                                                                                                                               CCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 86
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Pred. No. 0.31;
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RESULT 10
US-10-042-431-79
; Sequence 79, Application US/10042431
; Publication No. US20020182675A1
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US-09-954-456-1143
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LENGTH: 2838
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SOFTWARE: PatentIn ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US/PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/60/234,923 PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 10.3%;
Local Similarity 45.3%;
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                                                                                                                                   1104 GCGGCCGCGCCGCCGCCGCCCGC 1128
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                                                                                                                                                                            GCTGTCTGAACTCGTGTGCGCCTGC
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Pred. No. 0.31;
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; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Bos sp.
US-10-042-431-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 449, Application US/09759130B Publication No. US20030022279A1
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CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF THE STATE OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
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APPLICANT:
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APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
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PRIOR
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
FILE REFERENCE: MPI00-5350MNIM
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                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16
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                                  APPLICATION NUMBER: US 09/333,159
FILING DATE: 1999-06-14
APPLICATION NUMBER: US 09/596,194
FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/479,249 FILING DATE: 2000-01-07
APPLICATION NUMBER: US 09/342,364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GCCGACTTGGCGCATGGAAAACCGTGCTGTGTGTGTGTGCGCCTGCCATG 295
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Myers, Paul S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sharp, John D
Barnes, Thomas S
Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wrighton, Nicolas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leiby, Kevin R
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Pred. No. 0.33;
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; LENGTH: 5502
; TYPE: DNA
; ORGANISM: human
US-10-021-955-1
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US-10-021-955-1
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PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
                                            US-10-021-955-72
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LENGTH: 4308
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Best Local Similarity
Matches 94; Conserv
Sequence 72, Application US/100 Publication No. US20030039987A1
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                          Best
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PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/021,955
CURRENT FILING DATE: 2001-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Takashima, Hiroshi
TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lupski, James R
APPLICANT: Boerkoel, Cornelius F
APPLICANT: Takashima, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: P02086USi/10026309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3535 GTGTGCGATGACTCCTGGAGCCTGGCAG-----AGGCTGAGGTGGTGTGTCAGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3475 GGAGGAGACAGCGAGTGCTCAGGGCGGGTGGAGGTGTGGCACAACGGCTCCTGGGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CACTGCGAGGAGGCCAGCCTGGCCGAACACACACGTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC 180
                                                                                                                                   653 ACGCGTGCTTAGCCCGGCCCCGGCCCTGGACTGCCCCAGCGATCC 697
                                                                                                                                                                                                                            593 GCCCGGGACCGTGTCTGGCTACGAGATCAAGGGCCCGCGGGCCAAGGTGGCCAAGCTGGT 652
                                                                                                                                                                               78 GCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGC 122
                                                                                                                                                                                                                                                                      18 GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGC
                                                                                                                                                                                                                                                                                                                     60;
                                                                                                                                                                                                                                                                                                                                          Similarity
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                     Application US/10021955
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57.1%;
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RESULT 15
US-09-975-719-160
; Sequence 160, Application US/09975719
; Publication No. US20030022349A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Rahme, Laurence G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-10-021-955-75
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; Sequence 75, Application US/10021955

; Publication No. US20030039987A1
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; ORGANISM: Human
US-10-021-955-72
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Best Local Similarity
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LENGTH: 5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lupski, James R
APPLICANT: Boerkoel, Cornelius F
APPLICANT: Takashima, Hiroshi
TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
CURRENT ENVENTION: DOMEST: US/10/021,955
CURRENT FILING DATE: 2001-12-13
PRIOR APPLICATION NUMBER: US 60/255,217
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: Takashima, Hiroshi
TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
FILE REFERENCE: P02086US1/10026309
CURRENT APPLICATION NUMBER: US/10/021,955
CURRENT FILING DATE: 2001-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/255,217
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 93
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APPLICANT: Boerkoel, Corne
APPLICANT: Takashima, Hiro
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Local Similarity 57.1%;
nes 60; Conservative
                                                                                                                                                                                             653 ACGCGTGCTTAGCCCGGCCCCGGCCCTGGACTGCCCCAGCGATCC 697
                                                                                                                                                                                                                                                                              593 GCCCGGGACCGTGTCTGGCTACGAGATCAAGGGCCCGCGGGCCAAGGTGGCCAAGCTGGT 652
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                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 9; Pred. No. 0.34; 0; Mismatches 4
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Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 5502;
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Search completed: June Job time : 138 secs
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                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa US-09-975-719-160
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 160
LENGTH: 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361003
CURRENT APPLICATION NUMBER: US/09/975,719
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 60/066,517
PRIOR FILING DATE: 1997-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                        Local Similarity es 67; Conserv
                                                                            1005 CCTG 1008
                                                                                                                     264 CGTG 267
                                                                                                                                                         945 GGACGACGCCAAGATCAAGCGCAACCGCGAATTCATGAACGTCTTCCAGCAATTGCGCGC 1004
                                                                                                                                                                                                                                         885 CCTCTTCCCCGGGTATCCCGAGGGTTACTACGAGAACCACTTCCTGCATTCCTTCGAGCT
                                                                                                                                                                                                                                                                    204 GGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAAC
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                           10.2%;
54.0%;
                 2003, 07:36:45
                                                                                                                                                                                                                                                                                                                      Score 32.8; DB Pred. No. 0.33; 0; Mismatches
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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11:
12:
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Listing first 45 summaries
): //SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:

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*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:

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*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995_DAT:

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*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999_DAT:

*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA20000_DAT:

*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA20001_DAT:

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*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA20001_DAT:

*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001_DAT:

*/SIDS2/gcgdata/geneseq/geneseq/geneseqp-embl/AA2001_DAT:

*/SIDS2/gcgdata/geneseq/geneseq/geneseqp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

10	9	8	7	6	G	4	w	) N	ם	No.	Result
290	594.5	601	603	605	605	605	605	607	613	Score	
47.3	97.0	98.0	98.4	98.7	98.7	98.7	98.7	99.0	100.0	Match:	Query
144	118	117	117	117	117	117	117	117	117	Length	
23	23	23	23	23	23	23	23	23	23	DB	
AAU97551	AAU97554	AAI197555	AAU97559	AAU97558	AAU97557	AAU97556	AAU97553	AAU97560	AAU97552	ID	
Shigella flexneri	Synthetic cadmium/	Synthetic MerR che	Description								

443 443	38 40 41	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	28 29 30	222222222222222222222222222222222222222	11 12 14 15 16 17 18
72 72 72 72	73.5 73.5 73.5 72.5	77 76.5 76.5 76.5	78.5 78.5 78.5	88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	276 257 125 123 123 88.5 88.5 88.5
	12.0 11.9 11.8	· · · · ·			45.0 41.9 20.4 20.1 144 144
264 400 999 1388	244 510 352 225 933	340 475 671 1037 799	823 880 268 347 2664	299 299 130 130	144 159 135 135 138 138 296 296 299
22 22 19	22	222222	221	223 23 22 23 23 23 23 23 23 23 23 23 23	20 15 15 23 23 23 21
AAM80130 AAM79146 AAY73362 AAW56475	AAX 1/5/5 ABG11601 AAY57596 ABG16600 ABB60762	ABG06450 AABB1188 ABB49703 ABB649999 ABB58486	AAG29828 AAG29828 ABG15429 ABG12165 ABG02343	ABB72153 ABB7216 ABB72216 ABB7233 ABF2833 ABF28475 AAG29830	AAY01816 AAR49668 AAR49669 AAR49670 ABP38137 AAB56069 ABB72269 ABB72269 AAY76014 AAY76077
Human protein SEQ Human protein SEQ HTRM clone 2674047 Protein with Rho p	Human cytoskeletal Novel human diagno Murine Wnt-3a prot Novel human diagno Orosophila melanog	human zinc i ria mor human phila n	Arabidopsis thalia Arabidopsis thalia Novel human diagno Novel human diagno Novel human diagno		MerR protein which Protein product of Protein product of Protein product of Protein product of Staphylococcus epi Skin cell protein iso Murine EGF family Murine EGF family Skin cell protein

## ALIGNMENTS

RESULT 1 N-PSDB; ABK52207, ABK52213. Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; MerR. WPI; 2002-435437/46 Summers AO, 12-OCT-2000; 2000US-240465P. (UYGE-) UNIV GEORGIA RES FOUND INC 12-OCT-2001; 2001WO-US31819 18-APR-2002 WO200230962-A2. Synthetic. Synthetic MerR chelon variant. 13-AUG-2002 (first entry) AAU97552; AAU97552 standard; Protein; 117 AA. Caguiat JJ;

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CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC creyion for the protein to produce a recombinant host cell and culturing CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC inmobilised onto a solid support, is useful for concentrating heavy metal CC ions from contaminated environment waste streams or contaminated CC aqueous medium including biological fluids. The nucleic acid, when cc recombinantly expressed in enteric bacteria (which are nontoxigenic and CC elimination of mercuric ion from gastrointestinal tracts of animals or CC elimination of mercuric ion from gastrointestinal tracts of animals or CC elimination of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino CC invention. This sequence is one of the heavy metal binding proteins of termed chelons of the invention.

CC invention of the invention acids 1-107 of this protein.
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Best Local (
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                                                                                                                                                                                                                                                                                                   Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent catio;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU97560 standard; Protein; 117
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                                                   12-OCT-2001; 2001WO-US31819.
                                                                                                                                                                 WO200230962-A2
                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic cadmium/mercury ion binding chelon protein #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
12-OCT-2000; 2000US-240465P.
                                                                                                          18-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA;
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                                                                                                                                                                                                                                                                            binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 613; DB 23;
Pred. No. 3.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                            divalent cation;
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RESULT 3
AAU97553
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CC The nucleic acid encoding the chelon protein is useful for binding coding creditions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when criminated environment waste streams or concentrate the heavy metal ions from contaminated environment waste streams or concentrating heavy metal consistency is suitable for useful for concentration and cell-indicated environment waste streams or contaminated environment environment waste streams or contaminated environment environment with high affinity. The present amino cell-indicated environment environment
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new non-naturally occurring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention.
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                                                                                                  Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                           AAU97553 standard; Protein; 117 AA
                                                                                                                                                                                                                                  Synthetic cadmium/mercury ion binding chelon protein #1
                                                                                                                                                                                                                                                                                      13-AUG-2002 (first entry)
                                                                         heavy metal binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIALLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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WO200230962-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding

CC divalent mercuric ions, to take up, sequester and concentrate the heavy

CC metal ions from contaminated soil, ground water, hydroponic solutions or

CC immobilised onto a solid support, is useful for concentrating heavy metal

CC ions from contaminated environment waste streams or contaminated

CC aqueous medium including biological fluids. The nucleic acid, when

CC recombinantly expressed in enteric bacteria (which are nontoxigenic and

CC recombinantly expressed in enteric bacteria (which are nontoxigenic and

CC nonpathogenic), is sultable for use in the in vivo sequestration and

CC elimination of mercuric ion from gastrointestinal tracts of animals or

CC humans exposed to toxic metal ions such as mercury and/or cadmium. The

CC molecules of the invention are also useful in water treatment resins.

CC The nucleic acid of the invention is highly specific and binds divalent

CC cation such as mercury or cadmium with high affinity. The present amino

CC acid sequence represents one of a collection (AAU97550-AAU97560) of

CC This sequence is one of the heavy metal binding proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                              Synthetic cadmium/mercury ion binding chelon protein #4.
                                                                                                 13-AUG-2002
                                                                                                                                          AAU97556;
                                                                                                                                                                                 AAU97556 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2002
                                                                                                                                                                                                                                                                                            61 HCEEVSSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                     61 HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                 MTHCEEVSSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.7%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 605; DB 2:
Pred. No. 2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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AAU97557 ID AAU9 XX

AAU97557 standard; Protein; 117 AA

RESULT

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61

61 HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117

HCEEASSLAEHKLKDVREQMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117

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В
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                                                                                                                                                                                 Matches 115;
                                                                                                                  Best
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                              ions from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AAU97553-AAU97560) of synthetic cadmium/mercury ion binding chelon proteins of the invention which is the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a soild support, is useful for concentrating heavy metal inmobilised onto a soild support, is useful for concentrating heavy metal
                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing a protein in a host-cell, by infecting or transforming a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
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                                                                                                                  Local Similarity
                       1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT
MTHCEEASSLAEHKLKDVREQMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT
                                                                                                                                                                                                                                              sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Page 22; 42pp; English.
                                                                                                                                                                                                                              invention.
                                                                                                                                                                                 117 AA;
                                                                                           Conservative
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                                                                                                             98.7%;
98.3%;
                                                                                                           Score 605; DB 2
Pred. No. 2e-52;
                                                                                        Mismatches
                                                                                                                                     DB 23;
                                                                                        0;
                                                                                                                                Length 117;
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60
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                                                                                                                                                                                                                                                           CC which binds mercuric ions. The invention is useful for recombinantly comprising a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding contaminated soil, ground water and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or cirrigation water of waste streams. The DNA of the invention, when commobilised onto a solid support, is useful for concentrating heavy metal constrained environment waste streams or contaminated concentrating heavy metal conspathogenic), is suitable for use in the in vivo sequestration and conpathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and concentration of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. CC the nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino can be invented as one of the heavy metal binding proteins termed chelons of the invention.
                                                                                                                                              Query Match
Best Local
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant DNA molecule comprising a sequence encoding a chelon protein
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  61
                                                             MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                        MTHCEEASSLAEHKLKDVREKMADLARVETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                                                                                                                         115;
                                                                                                                                                                                                                                                invention.
                                                                                                                                              Similarity
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                                                                                                                         Conservative
                                                                                                                                            98.7%;
98.3%;
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                                                                                                                                          Score 605; DB 2
Pred. No. 2e-52;
                                                                                                                           Mismatches
                                                                                                                                                                 DB 23; Length 117;
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                                                                                                                           Indels
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                                                                                                                         Gaps
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Best Local Similarity
Matches 115; Conser

Conservative

2

Mismatches

DB 23;

Length 117; Indels

0;

Gaps

0

98.7%; 98.3%;

Query Match

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                                                                                                                                                          Comprising a protein in a host-cell, by infecting or recombinant DNA molecule comprising a sequence encoding a chelon protein

CC which binds mercuric ions. The invention is useful for recombinantly

CC producing a protein in a host-cell, by infecting or transforming a host

CC producing a protein in a host-cell, by infecting or transforming a host

CC cell capable of expressing a chelon coding sequence with a vector

CC comprising a promoter active in the host cell operably linked to a coding

CC region for the protein to produce a recombinant host cell and culturing

CC region for the protein to produce a recombinant host cell and culturing

CC the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding

CC divalent mercuric ions, to take up, sequester and concentrate the heavy

CC metal ions from contaminated soil, ground water, hydroponic solutions or

CC immobilised onto a solid support, is useful for concentrating heavy metal

CC ions from contaminated environment waste streams or contaminated

CC aqueous medium including biological fluids. The nucleic acid, when

CC compathogenic), is suitable for use in the in vivo sequestration and

CC nonpathogenic), is suitable for use in the in vivo sequestration and

CC compathogenic), is suitable for use in the in vivo sequestration and

CC nonpathogenic), is suitable for use in the in vivo sequestration and

CC molecules of the invention are also useful in water treatment resins.

CC The nucleic acid of the invention is highly specific and binds divalent

CC acido sequence represents one of a collection (AAU97553-AAU97560) of

CC synthetic cadmium/mercury ion binding chelon proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalen
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                                                                            Sequence
                                                                                                                             of the invention.
                                                                                                                                                   This sequence is one of the heavy metal binding proteins termed chelons
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Score 605; Db 2-
NO. 2e-52;
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В

MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT

MTHCEEASSLAEHKLKDVREKMADLARIETVLSELVCACHARKGNVSCPLIASLQGSSGT 60

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Which binds mercuric ions. The invention is useful for recombinantly cell capable of expressing a chelon coding sequence with a vector cell capable of expressing a chelon coding sequence with a vector cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding certain for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. Consider the recombinant host cell under conditions, where DNA is expressed in the recombinant mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when cell capable of the invention is useful for concentrating heavy metal constitution of mercuric ion from gastrointestinal tracts of animals or contaminated environment waste streams or contaminated cell mination of mercuric ion from gastrointestinal tracts of animals or contamination of mercuric ion from gastrointestinal tracts of animals or contamination of mercuric ion from gastrointestinal tracts of animals or contamination of mercuric ion from gastrointestinal tracts of animals or contamination of mercuric ion from gastrointestinal tracts of animals or concentration and cell action such as mercury and/or cadmium. The concentration are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino contamination of the heavy metal binding proteins of the invention.
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is one of the heavy metal binding proteins termed chelons
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CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding CC region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC inmobilised onto a solid support, is useful for concentrating heavy metal conservation and the component waste streams or contaminated contaminated environment waste streams or contaminated contaminated in enteric bacteria (which are nontoxigenic and conspathogenic), is suitable for use in the in vivo sequestration and conspathogenic), is suitable for use in the in vivo sequestration and conspathogenic), is suitable for use in the in vivo sequestration and conspathogenic).
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elimination of mercuric ion from gastrointestinal tracts
                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                             which binds mercuric ions.
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                                                                                                                                                                                                                                                                                                                                                                                                        contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Sim
hes 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVPCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                          DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.4%;
                                                                                                                                                                                                                                                                                           The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 603; DB 23; Pred. No. 3.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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or

8888888<del>8</del>8

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Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AA097553-AA097560) of synthetic cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or
                                                                                                                                                                        The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic cadmium/mercury ion binding chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU97554 standard; Protein; 118
                                                                                                                                                                                                                                                                                                            contaminated soil, water, aqueous
                                                                                                                                                                                                                                                                                                                            Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001; 2001WO-US31819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200230962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy metal binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU97554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000; 2000US-240465P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115;
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                                                                                                                                                                                                                                                                  Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 601;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                            medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 23; Length 117; 4.9e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ions from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AAU97563) of synthetic cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                             irrigation water;
biological fluid;
enteric bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97551 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-2002 (first entry)
                                                                                                                                                                                                                 Summers AO, Caguiat JJ;
                                                                                                                                                                                                                                                                                 12-OCT-2000; 2000US-240465P
                                                                                                                                                                                                                                                                                                                                                  18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                 WO200230962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy metal binding protein; MerR.
                                                                                                                                                                                  WPI; 2002-435437/46.
                                                                                                                                                                                                                                                 (UYGE-) UNIV GEORGIA RES FOUND
                                                                                                                                                                                                                                                                                                                12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 THCEEASSLVEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTHCEEASSLAEHKLKDVREK-MADLARMETVLSELVCACHARKGNVSCPLIASLQGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTHCEEASSLVEHKLKDVREKTMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             waste stream; contaminated aqueous medium;
gastrointestinal tract; chelon protein;
toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 594.5;
Pred. No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
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Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein useful for binding divalent cation mercury from the chelon protein the chelon protein

contaminated soil, water, aqueous medium including biological fluids

N-PSDB;

ABK52206

The present invention relates to a new non-naturally occurring

 ${\tt DNA}$  molecule comprising a sequence encoding a chelon protein mercuric ions. The invention is useful for recombinantly

Disclosure; Page 20; 42pp; English

which binds recombinant

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RESULT 11
AAXO1816
ID AAXO1816
ID AAXO1
AC AAXO1
AC AAYO1
AC AAYO1
XX Heavy
KW Heavy
KW Capac
KW Zinc;
KW Food.
XX Pseud
PN WO991
XX PSEUD
PN UO991
XX USERC
PA (BONT
PA (BONT
PA (JONE)
PA (UNBI
PA (UNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                    WPI; 1999-254424/21
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                                                                                                                  Van Der Lelie D,
                                                                                                                                           Berggren C, Bontidean I, Brown N,
Hobman J, Jakeman K, Johansson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9914597-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy metal ion selectivity; metal ion-specific affinity sensor; capacitance measurement; noble metal; self-assembling monolayer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MerR protein which has selectivity towards heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY01816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY01816 standard; protein; 144 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BERG/) BERGGREN C. (BONT/) BONTIDEAN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing
                                                                                                                                                                                                                                                                                                                                                                                            (JOHA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                     (CSOE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mercury; cadmium; copper; lead; environmental sample; medicine;
                                                                                                                                                                                                                                                                                                                                                                                        ) BONTIDEAN I.
) CSOEREGI E.
) JOHANSSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
56; Conserv
                                                                                                                                                                                                                                         MATTIASSON B.
MATTIASSON B.
UNIV BIRMINGHAM SCHOOL BIOLOGICAL SCI.
UNIV BIRMINGHAM SCHOOL BIOLOGISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97SE-0003315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-SE01638.
                                                                                                                  Wilson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 290; DB 23;
Pred. No. 3.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                               Corbisier
Lloyd J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                   P, Csoere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                               Csoeregi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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RESULT 12
AAR49668
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention. The specification describes a metal ion-specific, affinity sensor that measures capacitance. The sensor comprises a piece of noble metal to which are bound groups that bind specifically to selected heavy metal ions. These groups are bound to a self-assembling monolayer that covers at least 90%, more preferably at least 99% of the noble metal surface. The noble metal is a rod or piece of insulating material (91ass, quartz or silica) on which a noble metal is sputtered. The sensor is used for qualitative or quantitative detection of selected heavy metal ions in liquid samples, particularly of zinc, mercury, cadmium, copper and lead in e.g. environmental samples, medicines, foods and other products.
                                                Sequence
                                                                           used to transform other bacteria.
                                                                                         The mercury resistance genes can be used as selectable markers when
                                                                                                                        Disclosure; Page 2; 26pp; Japanese
                                                                                                                                                                   Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transform
                                                                                                                                                      Thiobacillus sp.
                                                                                                                                                                                                                   N-PSDB; AAQ58554.
                                                                                                                                                                                                                                   WPI; 1994-077131/10.
                                                                                                                                                                                                                                                                                                            17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                         17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR49668 standard; Protein; 159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein product of mercury resistance control gene merR(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                (DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                               (AKIT-) AKITA KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a protein that is selective towards heavy metal ions. It is used in the construction of the sensor of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 22-23; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capacitance sensor specific for heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity 93.0%;
                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                A
                                                                                                                                                                                                                                                                                                            91JP-0018338
                                                                                                                                                                                                                                                                                                                                            91JP-0018338
 41.98;
76.98;
Score 257; DB 15;
Pred. No. 7.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 276; DB 20;
Pred. No. 9.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                15;
                Length 159;
                                                                                                                                                                      in transformed
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Matches

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RESULT 14
AAR49670
ID AAR49
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AC AAR49
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                                                                                                                                                                                                                                Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                           Protein product of mercury resistance control gene merR(2).
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                               Disclosure; Page 3; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                      Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                              Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transform
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ58555
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-077131/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP06000083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Resistance; mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR49669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR49669 standard; Protein; 135 AA
          Thiobacillus ferrooxidans
                                                              Protein product of mercury resistance control gene merR(3).
                                                                                     16-SEP-1994 (first entry)
                                                                                                           AAR49670
                                                                                                                                 AAR49670 standard; Protein; 135
                              Resistance; mercury; selectable marker; Thiobacillus ferrooxidans; transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                               (AKIT-) AKITA KEN.
(DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 GDRAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 CEEAS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                       76
                                                                                                                                                                                                  2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THCREAAELASRHLASVQARLRELHRIEHALQKQLEACNSQQGNFSCPLIDSLR 129
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                           135 AA;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-0018338
                                                                                                                                                                                                                                 20.4%; Score 125; DB 15;
44.4%; Pred. No. 7.5e-05;
tive 13; Mismatches 17;
                                                                                                                                  A
                                                                                                                                                                                                                                                      Length 135;
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RESULT 15
ABP38137
ID ABP38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The mercury resistance genes can be used as selectable markers when used to transform other bacteria. % \left( 1\right) =\left\{ 1\right\} =\left\{ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP38137 standard; Protein; 138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ58556.
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                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis; open antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AKIT-) AKITA KEN.
(DOWA ) DOWA MINING CO LTD.
Disclosure; SEQ ID 2982; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 THCREAAELASRHLASVQARLRELHRIEYALQKQLEACKSQQGNFSCPLIDSLR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91JP-0018338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bush D;
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have

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Search completed: May 28, 2003, 10:27:55 Job time: 37 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USPTO web site.
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Ouery Match 47.1%; Score 289; DB 2; Length 144; Best Local Similarity 96.6%; Pred. No. 8e-20; Matches 56; Conservative 0; Mismatches 2; Indels 0; Gaps 0	RESULT 2 S51706 S51706 regulatory protein merR - Alcaligenes faecalis C;Specles: Alcaligenes faecalis C;State: Change 20-Sep-1999 C;Accession: S51706 A;Reference number: Squence conservation between regulatory mercury resistance gene: A;Reference number: S51703 A;Rolecule type: DNA A;Residues: 1-144 <osb> A;Cross-references: EMBL:Z33484; NID:g607038; PIDN:CAA83892.1; PID:g607039 C;Superfamily: transcription repressor glnR</osb>	RESULT 1  S09527  regulatory protein merk - plasmid NR1  C; Species: plasmid NR1  A; Barrineau, P; Gilbert, P; Jackson, W.J.; Jones, C.S.; Summers, A.O.; Wisdom, J. Mol. Appl. Genet. 2, 601-619, 1984  A; Title: The DNA sequence of the mercury resistance operon of the IncFII plasmid A; Reference number: S09447; MUID:85159407; PMID:6530603  A; Recession: S09527  A; Molecule type: DNA  A; Residues: 1-144 <bar> A; Residues: 1-144 <bar> A; Residues: 1-144 <bar> A; Cross-references: EMBL:KO3089; NID:g150389; PIDN:AAB59072.1; PID:g455296  C; Genetics: A; Genome: plasmid  C; Superfamily: transcription repressor glnR  Query Match  Best Local Similarity 96.6%; Pred. No. 7.2e-20; Matches 56; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  Matches 56; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  Qy 2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSAG 59   </bar></bar></bar>	30 76.5 12.5 671 2 AFI294 31 76 12.4 674 2 T22733 32 75 12.2 141 2 AE0029 33 75 12.2 2442 2 T08621 34 73.5 12.0 671 2 AJ9666 35 73 11.9 352 2 AJ9532 36 72 11.8 357 2 A71295 37 72.5 11.8 466 2 T29353 37 72.5 11.8 466 2 T29353 37 72.5 11.8 694 2 T08896 40 72 11.7 197 2 T34551 41 72 11.7 2094 2 S33124 42 71 11.6 132 2 T45509 ALIGNMENTS  Appothetical prote methyl-accepting the mother of the methyl-accepting the methyl-accepting the mother of the methyl-accepting the meth
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C;Species: Pseudomonas sp.
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A; Residues: 1-144 < OSB>
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A; Accession: S51749
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                                                                                                         A;Cross-references: EMBL:Z33490; NID:g607153; PIDN:CAA83898.1; PID:g607154
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Pred. No. 6e-19;
                    Score 276; DB 2; Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between regulatory mercury resistance genes from me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 144;
                                        Length 144;
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Indels
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0;
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Gaps
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C;Species: Xanthomonas sp.
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999 C;Accession: S32798; S70142
R;Kholodil, G.Y.; Yurieva, O.V.; Lomovskaya, O.L.; Gorlenko, Z.M.; Mindlin, J. J. Mol. Biol. 230, 1103-1107, 1993
A;Title: Tn5053, a mercury resistance transposon with integron's ends. A;Reference number: S32795; MUID:93253772; PMID:8387603
A;Accession: S32798
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L03729; NID:g1019671; PIDN:AAA98396.1; PID:g154910
A;Experimental source: plasmid RP1; transposon Tn5053
R;Kholodii, G;Y.; Mindlin, S.Z.; Bass, I.A.; Yurieva, O.V.; Minakhina, S.V.; Nikiforo Mol. Microbiol. 17, 1189-1200, 1995
A;Title: Four genes, two ends, and a res region are involved in transposition of Tn50
A;Reference number: S70140; MUID:96130850; PMID:8594337
A;Accession: S70142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hobman, J.; Kholodii, G.; Nikiforov, V.; Ritchie, D.A.; Strike, P.; Gene 146, 73-78, 1994
A;Title: The sequence of the mer operon of pMER327/419 and transposon A;Reference number: I39574; MUID:94341572; PMID:8063107
A;Accession: I39574
                                                                                    A; Mobile element: transposon Tn5053 C; Superfamily: transcription repres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-144 <KHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: merR C;Superfamily: transcription repressor glnR
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C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999
C;Accession: I39574; S37035
                                                                                                                                                A;Gene: merR
                                                                                                                                                                                                       A;Cross-references: EMBL:L40585; NID:g710572; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-144 <KH2>
                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-144 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 THCEEASSLAEHKLKDVRERMADLARMEAVLSDLVCACHARKGNVSCPLIASLQGKKEPR 139
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53; Conserv
                                                                                       transcription repressor glnR
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82.8%;
44.5%;
82.8%;
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Pred. No. 2.7e-18;
   Score 273; DB 2;
Pred. No. 2.7e-18;
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                              DB 2; Length 144;
                                                                                                                                                                                                          PIDN:AAA98322.1; PID:g710575 to the EMBL Data Library, May 1995
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Conservative

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Mismatches

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RESULT 10
S51703
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N;Alternate names: mer operon regulator
C;Species: Pseudomonas fluorescens
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: S37044
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A;Residues: 1-144 <HOB>
A;Cross-references: EMBL:223095; NID:g397617; PIDN:CAA80641.1; PID:g397618
C;Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, June 1993
A;Description: The nucleotide sequence of the mer operon of pMJ100 and transposon ends
A;Reference number: S37035
regulatory protein merR - Acinetobacter calcoaceticus (isolate SE11 and SE12)
                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Description: Sequence conservation between regulatory mercury resistance genes from me
A:Reference number: S51703
A:Accession: S51756
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A; Residues: 1-144 < OSB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory protein merR - Comamonas testosteron1
C:Species: Comamonas testosteron1
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                                                                                                    140 SADA 143
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                                                                                                                                       62 CEEA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.; Kholodii, G.; Nikiforov, V.; Ritchie, D.A.; Strike, P.; Yurieva, O.
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82.8%;
                                                                                                                                                                                                                                               3; Mismatches
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Pred. No. 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 273; DB 2; Length 144; Pred. No. 2.7e-18;
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                                                                        RESULT 12
S51705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S51721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulatory protein merR - Enterobacter cloacae C; Species: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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C;Superfamily: transcription repressor glnR
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A; Residues: 1-151 <OSB>
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                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                             138 L-AASARGSH 146
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                                                                                                                                                                                62 CEEASSLAEH 71
                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                              l Similarity 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
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                                                                                                                                                                                                                                                                                                            44.0%;
81.4%;
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81.4%;
                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                            Score 269.5; DB 2
Pred. No. 5.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 269.5; DB 2
Pred. No. 5.9e-18;
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regulatory protein merR - Klebsiella oxytoca

C;Species: Klebsiella oxytoca

C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999

C;Accession: S51705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z33486; NID:g607073; PIDN:CAA83894.1; PID:g607074 C;Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
C;Accession: S51721
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A;Variety: isolate SE11; isolate SE12
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C;Accession: S51703; S51704
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                                                                                                                                                                                                                                                                                                                                                                                       80 THCEEASGLAEHKLKDVREKMADLARMEAVLSELVCACHARKGNVSCPLIASLQ--DGTK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.
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R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A. submitted to the EMBL Data Library, May 1994
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A; Accession: S51705
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A; Residues: 1-151 <OSB>
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C;Species: Agrobacterium radiobacter
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
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A; Genome: plasmid
C; Superfamily: transcription repressor glnR
C; Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                 merR protein - Escherichia coli plasmid pDU1358
C;Species: Escherichia coli
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Sep-1999
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A; Accession: S51707
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R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.
submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                  A;Title: Mercury operon regulation by the merR gene of the organomercurial resistance syA;Reference number: A33858; MUID:89327136; PMID:2666393
A;Accession: A33858
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R;Nucifora, G.; Chu, L.; Silver, S.; Misra, T.K.
J. Bacteriol. 171, 4241-4247, 1989
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A; Residues: 1-151 <OSB>
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                                                                                                                            A; Molecule type: DNA
A; Residues: 1-144 < NUC>
                                                                                C; Genetics:
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                                                   plasmid
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81.4%;
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Pred. No. 5.9e-18;
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Pred. No. 1.1e-17;
2; Mismatches 9; Indels 3
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mol. Microbiol. 5, 2707-2718, 1991
A;Title: The merR regulatory gene in Thiobacillus ferrooxidans is spaced apart from A;Reference number: S18584; MUID:92140035; PMID:1779760
A;Accession: S18590
A;Accession: S18590
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                               A;Cross-references: EMBL:x57326; NID:g48150; PIDN:CAA40603.1; PID:g48157 C;Superfamily: transcription repressor glnR
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Search completed: May 28, 2003, 10:29:15 Job time: 18 secs
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A; Residues: 1-135 <INO>
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Best Local Similarity
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Best Local :
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                                                                                                                             2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQ
                                                                                                                                                                    24;
                                                                                                                                                                                          Similarity
                                                                                                                                                                  20.4%; Score 125; DB 2; Length 135; ilarity 44.4%; Pred. No. 0.00012; Conservative 13; Mismatches 17; Indels
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92.7%;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the rotal score distribution
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Gapop 10.0 , Gapext 0.5
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613
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J. MOI. Appl. Gene -! FUNCTION: MEDI TRANSCRIPTION WHEN MERCURY I AND BECOMES A BOUND TO THE -! SIMILARITY: BE REGULATORS. This SWISS-PROT en between the Swiss the European Bioin use by non-profi modified and this entities requires or send an email t	UENCE FROM CIES-S.f. LINE-851 rineau Prineau Polom S.; e DNA See	SEQUENCE FROM N.A. SPECIES=S. typhi; ST SPECIES=2153447; I PAIKHIL J. DOUGH Churcher C., Munga. Baker S., Basham D Cronin A., Davis P Feltwell T., Hamlil Krogh A., Larsen T Quail M., Rutherfo; Whitehead S., Barro "Complete genome se enterica serovar T Nature 413:848-852	APR-1988 APR-1988 APR-1988 APR-1988 APR-1988 CULTC TO CUL	ri R_SALTI	68 68 67 67 67
ppl. Genet. Fig. 1. G	FROM N.A. S.flexneri; B5159407; Pu 1 P., Gilber .; sequence of	OM N.A. Typhi, STR yphi, STR yphi, STR yphi, STR Davis D. Nungall asham D. Hamlin asham D. Hamlin arsen T.S utherford barrel enome server covar Typh 648-852(2)	He (Rel. 07, 18 (Rel. 07, 18 (Rel. 07, 12 (Rel. 41, 12 (R	ST	11.1 11.1 11.1 11.1 11.1 11.1 11.1 11.
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	IncFII 0603; ckson w	; PLASMI 77608; S K.D.; entley S R.M. Do e A.; Hi er S.; M monds M.	sequence annotatio regulator remains IncFII NR gamma subd	ALIGN PRT;	MYH7_PAPHA HEM1_NEIGO HEM1_NEIMB HEM1_NEIMB HEM1_NEIMB HF7_PASMU MYH7_HUMAN MYH6_RAT PPD3_RART PPD3_RAFT DHSB_SCHPO TRPE_BACPU Y552_HUMAN
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RE PT OR A A I I I I I I I I I I I I I I I I I	; mers	ckard D, Seba ., Seba inerton Farrar S., Jag P., Par yvens K.	Enterobacteriaceae;		P11778 Q9zhd6 Q9zhd6 Q9zhd94 P56994 P57873 P13540 P12883 P12883 P02563 P57741 P21911 P18267 O60299
OF MERCURY PRESSES REGION; SINGLE ION E REMAINING IONAL IONAL TONAL TONA	A.O.,	, Wain J., P., P., J., J., Pels K., TYY C.,	O O		papio hamad neisseria g neisseria m neisseria m neisseria m pasteurella measocricetu homo sapien rattus norv arabidopsis schizosacch bacillus pu homo sapien

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                                                                     Shewchuk L.M., Verdine G.L., Nash H., Walsh C.T.;

"Mutagenesis of the cysteines in the metalloregulatory protein MerR
indicates that a metal-bridged dimer activates transcription.";

Biochemistry 28:6140-6145(1989)

-I- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY
RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES
TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION;
WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINCLE ION
AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING
BOUND TO THE MER SITE.
                                                                                                                                                                                                                                                                                                                                                 Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Barnes W.M., Haberstroh L., Silver S.; "Mercuric ion-resistance operons of plasmid R100 and transposon Tn501: the beginning of the operon including the regulatory region and the first two structural genes."; Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa, and Pseudomonas fluorescens. Plasmid pVS1.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric resistance;
Mercury; DNA-binding; Plasmid; Transposable element;
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EMBL; K03089; AAB59072.1; -.
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the \Xi
                                                                                                                                                                                                                                                                      Osborn A.M., Bruce K.D., Submitted (DEC-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPOSON-Tn501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas
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                                                          SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                            REGULATORS.
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HG(2+).
HG(2+).
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Pred. No. 1.9e-20;
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Best Local (
                                                                                                                                                                              Nucifora G., Chu L., Silver S., Misra T.K.;

"Mercury operon regulation by the merr gene of the organomercurial resistance system of plasmid pDU1358.";

J. Bacteriol. 171:4241-4247 (1989).

-i- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING BOUND TO THE MER SITE.
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SMART; SM0042; HTH_MERR; 1.

PROSTITE, PS00552; HTH_MERR.FAMILY; 1.

Transcription regulation; Activator; Repressor; Mercuric resistance; Mercury; DNA-Dinding; Plasmid; Transposable element.

Mercury; DNA-Dinding; Plasmid; Transposable element.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
Mercuric resistance operon regulatory protein
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                                                                                                                                  REGULATORS.
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Pred. No. 3.9e-19;
2; Mismatches 2
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C->S: ABOLI
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Best Local
                                                                                                                                                                                                                                                                                 OPETON FROM Staphylococcus aureus plasmid p1258.";
PTOC. Natl. Acad. Sci. U.S.A. 84:5106-5110(1987).
-I- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
             PRINTS; PR00040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
                                           InterPro; IPR000551;
Pfam; PF00376; merR;
                                                                      EMBL; L29436; AAA98241.1; -. PIR; A29504; A29504.
                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. (
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87260937; pubMed=3037534;
Laddaga R.A., Chu L., Misra T.K., Silver S.;
"Nucleotide sequence and expression of the mercurial-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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P22874;
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Transcription regulation, Activator; Repressor; Mercuric resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mercury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A33858; A33858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M24940; AAA98221.1; -.
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                                                                                                                                                                                                                                       BOUND TO THE MER SITE.
SUBUNIT: HOMODIMER.
SUBURITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                 REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THCEEASSLAEHKLQDVREKMTDLARMETVLSELVFACHARQGNVSCPLIASLQG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
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117
126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.4%;
92.7%;
                                                        HTH_MerR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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HG(2+).
HG(2+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05FBF5224B89C052 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                       Helmann J.D., Ballard B.T., Walsh C.T.; "The MerR metalloregulatory protein binds mercuric ion tricoordinate, metal-bridged dimer.";
                                                                                                                                                                                                                                                                                                                                                                                 Gram-negative bacteria control transcription of mercury
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89123021; PubMed=2492496;
Helmann J.D., Wang Y., Mahler I., Walsh C.T.;
"Homologous metalloregulatory proteins from both Gram-positive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89123092; PubMed=2536669; Wang Y., Moore M., Levinson H.S., Silver S., Walsh C., Mahler I.; "Nucleotide sequence of a chromosomal mercury resistance determination a Bacillus sp. with broad-spectrum mercury resistance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MERN.
Bacillus sp. (bulles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel.
01-AUG-1991 (Rel.
01-OCT-1993 (Rel.
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METAL
                                                                                                                                                                                                                                                                                                                                                                           operons.
                                                                                                                                                                                                                                                                           Science 247:946-948(1990)
                                                                                                                                                                                                                                                                                                                            MEDLINE=90161989; PubMed=2305262;
                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mercuric resistance operon regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P22853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 CKDMYAFTVQKTKEIERKVQGLLRIQRLLEELKEKCPDEKAMYTCPIIETLMG 131
                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 171:222-229(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 171:83-92(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
                                                                                                                                                                                                FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING BOUND TO THE MER SITE.
                                                                                                                                                                         SUBUNIT: HOMODIMER. SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                               REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain RC607).
rmicutes; Bacillales;
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    Created)
    Last sequence u
    Last annotation

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30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HG(2+).
HG(2+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HG(2+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDC1A852621D4F82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 135
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                                                                                                                                                                                                               WHILE REMAINING
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                                                                                                                                                                                                                                                                                                                                                                                        resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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PIR; A32227; A32227 PIR; A32239; A32239

InterPro;

IPR000551;

HTH\_MerR

EMBL; AF138877; AAA83973.1;

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RESULT 6
ZNTR_ECOLI
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p36676;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
2n(II)-responsive regulator of zntA.
ZNTR OR B3292 OR Z4662 OR ECS4157.
Escherichia coli, and
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
MUTAGEN
                                                                                                                       STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-94341562; PubMed-8063098;

Christie G.E., White T.J., Goodwin T.S.;

A merk homologue at 74 minutes on the E.

Gene 146:131-132(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00376; merR; 1
                                                                                                                                                                                                                                                                                                                                    MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collador-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
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                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                              Nature 409:529-533(2001).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZNTR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562, 83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRDMYDFTILKIEDIQRKIEDLKRIERMLMDLKERCPENKDIYECPIIETL 129
                                                                                                                                                                                                                                                                                                                           Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
123
132 AA;
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114
123
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79
114
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31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Enterobacteriaceae;
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HG(2+).
HG(2+).
C->A, H: LOSS OF HG
C->A, H: LOSS OF HG
C->A, H: LOSS OF HG
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->A: LOSS OF HG BINDING.
->A, H: LOSS OF HG BINDING.
6557FBF1FB95B635 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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       Yasunaga T.
                       Tobe
                                     Yokoyama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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SQ TWREET BREET BR
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Best Local
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ECOGENE; EG11959; ZDICR.
ECOGENE; EF1000551; HTH_MERR.
Interpro; IPR000551; HTH_MERR.
PF00376; merr; 1.
SMART; SM00422; HTH_MERR; 1.
SMART; SM00422; HTH_MERR, FAMILY; 1.
PROSITE; PS00552; HTH_MERR, FAMILY; 1.
PROSITE; PS00555; HTH_MERR, FAMILY; 1.
PROSITE; PS00550; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; pubMed=11859360; wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat W., Hayles J., Baker S., Basham D., Bowman S., Srowh D., Brown S., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UTK5; O13313; Q9UTT8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Abnormal long morphology protein 1 (Sp8).
ALMI OR SPAC1486.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L29458; AAA24773.1; -. EMBL; U18997; AAA58089.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99157592; PubMed=10048032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
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Moule S.,
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31.0%;
Mungall K., Murphy L.,
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RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fitzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RI The genome sequence of Schizosaccharomyces pombe.";

RI Nature J. L., 271. 2807/2002
                                                                                                                                                              Matches
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Large-scale screening of intracellular protein localization in livin fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-968 h90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jimenez M., Petit T., Gancedo C., Goday C.;
"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20123449; PubMed=10660053;
Jimenez M., Petit T., Gancedo C., Goday C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oliver K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL133357; CAB62414.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20223868;
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192 EILVQEKSALVSDLASLQSDHSKVCEKL-EVSSRQVQDLEKKLAGLAQQNTELNEKIQLF
                                        48
                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOKINESIS.
                                                                                                                      EEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVS-------
                                      -----CPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCAC 97
                                                                                QEQSKIASEQLSIAKDQIEALQNENSHLGEQVQSAHQALSDIEERKKQHMFASSSSRVKE
                                                                                                                                                                                                                                                                                                                                                                                                                              AB028012;
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                                                                                                                                                                               Similarity
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443
542
804
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1601
1727
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                          ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                              BAA87316.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB65416.1;
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463
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1106
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19.5%;
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                                                                                                                                                            26;
                                                                                                                                                                                                                                                             COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALT_INIT.
                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                  Score 77;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                          F820BF8D9C132644 CRC64;
                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                  Length 1727;
                                                                                                                                                            Indels
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Query Match
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Thes 15; Conserve
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
Transcriptional regulator cueR (Copper efflux regulator) (Copper export regulator)
EXPORT FOR VEGR OR VCO974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUER_VIBCH
                                                                                                                                                                                                                                                           PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Srivastava B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae.
                                                                                                                                                                                                       Complete
                                                                                                                                                                                                                                Transcription regulation; Activator; DNA-binding; Copper;
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00376; merR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ277893; CAC21398.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype Ol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                               DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000551; HTH_MerR.
                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; VC0974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 EQKRSNYS 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in response to increasing copper concentrations (By simila SUBUNIT: Homodimer (Potential).

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

DOMAIN: It contains a N-terminal DNA binding region and a terminal metal binding region (By similarity).

SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL REGULATORS. CUER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Regulates the transcription of the copA and cueO genes It detects cytoplasmic copper stress and activates transcription in response to increasing copper concentrations (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                        AE004179; AAF94136.1;
                                                                                                                                                                                                       proteome.
                                                                                                                                              139 AA;
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                 15693 MW;
                                                         12.5%;
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                              15;
                                                         Score 76.5;
Pred. No. 1
                                                                                                                                                                            H-T-H MOTIF (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                    84CEDED9D411B012 CRC64;
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
                                                                                       DB 1;
                                 17;
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                                                                                       Length 139;
                                 Indels
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                                 Gaps
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11 AEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTHC 62

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84

AQEKWQEISRKLSELTMIKQQLEEWIASCPGDQGS-DCPIIEQLKG----HC

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ALD DETERMINED TO SERVICE OF SERV
                                                                                                                                                             RX KEDLINE-2019606; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Golie R.F.,
RA Amanatides P.G., Scherer S.E., If P.W., Hoskins R.A., Galle R.F.,
RA Baradon R.C., Wortman J.R., Xandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Wortman J.R., Xandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarojlu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Belshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktarojlu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchar A., Deng Z., Mays A.D., Devi I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA McIsulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIsulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Harris K., Kemington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylraska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang S. M., Woodsage T., Worley R., Smith T.,
RA Harris R., Zhong F.R., Zhong W., Zhang G., Zhou X., Zheng L.,
RA Harris R., Zhong F.N., Zhong W., Zhon W., Zhong S., Yao Q.A.,
RA Harris R., Zhong F.N., Zhong W., Zhon W., Zhong S., Yao Q.A.,
RA Harris R., Zhong F., Zhong M., Zhon W., Zhong S., Yao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

MCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel, tissue-specific integrin subunit, beta nu, expressed in the midgut of Drosophila melanogaster.";
Development 118:845-858(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q27591; Q9VIG7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yee G.H., Hynes R.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94357079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin beta-nu precursor.
BETA-INT-NU OR CG1762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TBN_DROME
                                                                                FUNCTION: PROBABLY PLAYS A ROLE IN CELL ADHESION.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endoderm;
LOCATION: Type I membrane protein.
BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8076521;
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                                                                                                                                              Y355_HUMAN
                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00011; EGFLAMININ.
ProDom; PD001811; Integrin_B; 1.
SMART; SM00181; EGF; 1.
SMART; SM00187; INB; 1.
SMART; SM00423; PSI; 1.
SMART; SM00327; VWA; 1.
                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Hypothetical protein KIAA0355.
                                                                                                                   015063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
NCBI_TaxID=9606;
                                                     KIAA0355.
                                                                                                                                  Y355_HUMAN
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00022; EGF_1; UNKNOWN PROSITE; PS01186; EGF_2; UNKNOWN PROSITE; PS00243; INTEGRIN_BETA; PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0010395; beta-Int-nu.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003669;
HSSP; P05106; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          integrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                 547 YTGPFCECRECL-----DCDEKLAD-----CFC----GQCVCKYGWS 579
                                                                                                                                                                                                                                                   495 TYCNCPTDATNVTSNEALLQKCRQPFSDKS----TSELVCSNH---GDCDCGTCLCDPG
                                                                                                                                                                                                                          57 SSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWS 111
                                                                                                                                                                                                                                                                2 THCE---EASSLAEHK--LKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00362;
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002369; Integrin_B.
IPR001169; Integrin_bet
IPR002049; Laminin_EGF.
IPR003659; Plexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                             26
27
799
27
725
26
746
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17
799
3
167
409
505
655
680
701
701
90841 MW;
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                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF53952.1; -.
                                                                                                                                                                                                                                                                                                                     12.3%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin_B.
Integrin_beta_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                        Score 75.5; D
Pred. No. 9.5;
.5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .
E -> G (IN REF. 1).
V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTEGRIN BETA-NU.
EXTRACELLULAR (POTENTIAL)
             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                             351869D523F07DEB CRC64;
                                                                                                                                 1070
                                                                            update)
                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                Length 799;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 11
WN3A_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
WNT-3A protein precursor.
WNT3A OR WNT-3A.
                                                                                           development -- restricted temporal and spatial patterns in the developing neural tube."; Genes Dev. 5:381-388(1991).
-- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein 50MAIN 551 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Mrediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WN3A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                              Roelink H., Nusse R.;
"Expression of two members of the Wnt family during mouse
                                                                                                                                                                                                               MEDLINE=91160971; PubMed=2001840;
                                                                                                                                                                                                                                    TISSUE-Embryo;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 MKEAGCYNGITSRDDFPVTEVLNQVCPSTW 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 CSQSAAIPEHQLKELNIKIDSALQAYKIALESLGHCEYAMKAGFHLNPKAIEASLQGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 THCEEASS-----------LAEHKLKDV--REKMADLARMET-VLSEL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CEEASSLAEHKLKDVREKMADLARMETVLSELVCAC-HARKGNVSC---PLIASLQGSSG 59
             extracellular matrix.
TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE (DEVELOPING
                                                SUBCELLULAR LOCATION: Possibly secreted and associates with the
                                                                                 CELL-CELL SIGNALING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --CSEAEAQQTGRRQTPPQPMQCELPTVPVQIGSHFLKGVSFNESAADNLKLKTHTMLQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB002353; BAA20812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1070 AA; 116047 MW; 2D35C127C5EBA2F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555
700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%;
                                                                                 DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVSCPSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PRO.
                                                                                 MORPHOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                 DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                               ROLES IN
                                                                                 NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
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AND MESENCHYME TISSUE SURROUNDING THE UMBILICAL

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SO TITE
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20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALR_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALR_TREPA
Q56346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
            "Partial sequence of alanine racemase from Treponema pallidum.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Provides the D-alanine required for cell wall
                                                                                                                                                                                                  MEDLINE=98332770; pubMed=9665876; Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alanine racemase (EC 5.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:98956; Wnt3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X56842; CAA40173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Developmental protein; Glycoprotein; Signal; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000970; Wnt_grthfactor.
Pfam; PF00110; wnt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                Steiner B.M., Rodes B.;
                                                                                 STRAIN-Nichols
                                                                                                                                                   spirochete.
                                                                                                                                                          "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                           STRAIN=Nichols
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=160
                                                                                                                                                                                                                                                                                                                                                                                                                                ALR OR TP0681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                 SEQUENCE OF 1-198 FROM N.A.
                                                                                                                                   Science
                                                                                                                                                                                     Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SAMNRHNNEAGRQAIASHMHLKCKCHGLSGSCEVKTCWWSQPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 SELVCACHARKGNVSCPLIASLQGSSGT-----HCE---EASSLAEHKLKDVREKMADL- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
biosynthesis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ARMETVLS--ELVCACHARKGNVSCPSA-WSHPQF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAAICGCSSR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR01349; WNTPROTEIN.
                                                                                                                                   281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298
352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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25.0%;
                                                                                                                                                                                                                                                                                                                                                                                             Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQGSPGEGWKWGGCSEDIEFGGMVSREFADARENRPDAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; 7ADFC5B38A8EFF63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNT-3A PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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IRRAL PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COMPONENT OF THE EXOSOME 3->5 EXORIBONUCLEASE COMPLEX.

REQUIRED FOR THE 3' PROCESSING OF THE 7S PRE-RNA TO THE MATURE
5.8S RRNA. HAS A 3'-5' EXONUCLEASE ACTIVITY (By similarity).

-i- SUBUNIT: COMPONENT OF THE EXOSOME MULTIENSYME RIBONUCLEASE COMPLEX

COMPOSED OF AT LEAST 11 PROTEINS: RRP4, RRP40, RRP41/SK16, RRP42,

RRP43, RRP44/DIS3, PM/SCL-75, RRP46, CSL4 AND PM/SCL-100 (ONLY IN
                                                                                                                                                                                                                                                                                       ARP41.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Exosome complex exonuclease RRP41 (EC 3.1.13.-) (Ribosomal RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                            processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001242; AAC65644.1; ALT_INIT.
EMBL; U57756; AAB17466.1; ALT_INIT.
HSSP; P10724; 1BD0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RR41_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fam; PF00842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000821; Ala_racemase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 CP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
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COFACTOR: Pyridoxal phosphate (By similarity).
PATHWAY: Along with D-alanine--D-alanine ligase, it makes
D-alanine branch of the peptidoglycan biosynthetic route.
SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Į
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEASSLAEHKLKDVREKMADLARMETVLSE-----LVCACHAR----KGNV-----SCP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVQMVCATPGLHLEGVCTHFSVAD----SVRAE--DLQYTEMQRAHFMHCVQYIRKSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIASLQGSSGTHCEEAS---SLAEHKLKDVREKMADLARMETVLSELV-CACHARKGNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR00492; alr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridoxal phosphate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALARACEMASE.
                                                                                                                                                                                                                                                                                                                                                                                                                               41).
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40312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
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25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72.5; D
Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).

CATALYTIC BASE SPECIFIC TO L-ALANINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96387BFF1EAD0913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASE; 1.
Cell wall; Peptidoglycan synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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   Query Match
Best Local
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Best Local
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099871;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                     EMBL; X99270; CAA67665.1; ... Genew; HGNC:12270; TREX2.
                                                                                                                                          the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                MEDLINE-97254469; PubMed-9099879;
Esposito T., Ciccodicola A., Flagiello L., Matarazzo M.R.
Migliaccio C., Cifarelli R.A., Visone R., Campanile C.,
Mazzarella R., Schlessinger D., D'Urso M., D'Esposito M.;
"Expressed STSs and transcription of human Xq28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; PF01138; RNase_PH; 1.
Pfam; PF03725; RNase_PH_C; 1.
Exosome; Hydrolase; Nuclease;
Nuclear protein; RNa-binding;
SEQUENCE 245 AA; 26249 MW;
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                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
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32; Conserv
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                                                      33582 MW;
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Score 72; 1
Pred. No. 7
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                                                      079BD40D8A56F45E CRC64;
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Matches

Similarity

32.7%;

Conservative

11;

Mismatches

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Indels

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Gaps

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RESULT 15
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"tpr homologues activate met and raf.";

Oncogene 2:617-619(1988).

-i- function: Component of the cytoplasmic fibrils of the nuclear pore complex implicated in nuclear protein import. Its amino terminus is involved in activation of oncognic kinases.

-i- Subcellular location: Cytoplasmic Surface of the nuclear pore complex. The assembly of the NPC is a Stepwise process in which the complex is a sasembly of the NPC is a Stepwise process in which the complex. The assembly of the NPC is a Stepwise process in which the components, including peripheral structures assemble after other components, including p62.

-i- tissue specificity: Highest in testis, lung, thymus, spleen and brain, lower levels in heart, liver, and kidney.

-i- debase: involved in tumorigenic rearrangements with the met, trk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95096166; PubMed-7798308;
Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T.,
Saphire A.C.S., Mitchell P.J., Copper C.S., Aebi U., Gerace L.;
"Tpr, a large coiled coil protein whose amino terminus is involved activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34,
16-OCT-2001 (Rel. 40,
Nuclear protein; Transport.
DOMAIN 78 360
DOMAIN 422 571
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
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Mitchell P.J., Cooper C.S.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                           MIM; 189940; -.
Coiled coil; Proto-oncogene; Chromosomal translocation;
                                                                                             PIR; S00928; S00928.
Genew; HGNC:12017; TPR.
                                                                                                                                     EMBL; X66397; CAA47021.1; -. EMBL; Y00672; CAA68681.1; -.
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POLY-ASP.
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Search completed: May 28, 2003, 10:28:14
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1: sp_bacteria
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5: sp_inverteb;
6: sp_manmal:*
7: sp_mhc:*
8: sp_page:*
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11: sp_rodent:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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LT 2 90 Q44190 Q44190;	Best Local Similarity Best Local Similarity Matches 56; Conserv 2 THCEEASSLAEHKI	Submitted ( EMBL; AJ422 Plasmid. NON_TER SEQUENCE	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TRANSPOSON-TN21 HC Kholodii G.Y., Gor "Distribution of d bacteria.";	MERR. Pseudomonas flu Plasmid pKLH22. Bacteria; Prote Pseudomonas. NCBI_TaxID=294;	LT 1 29 28 28 28 28 28 28 28 27 20 20 20 20 20 20 20 20 20 20 20 20 20
PRELIMINARY;	ilarity 96.6%; Conservative 1 SSLAEHKLKDVREKMADL	<b>a</b> "	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TRANSPOSON-TN21 HOMOLOGUE; Kholodii G.Y., Gorlenko Z.M., "Distribution of distinct mic bacteria.";	6 0 5 E	PRELIMINARY; (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21, (Fragment).
PRT;	Pred. No. 5e- 1; Mismatches 1; ARMETVLSELVCA	MBL/GenB C51422	Mindlin rovarian		PRT; 124 / Created) Last sequence Last annotatio
144 AA.	al Similarity 96.68; Pred. No. 5e-21; 56; Conservative 1; Mismatches 1; Indels 0; Gaps 56; Conservative 1; Mismatches 1; Indels 0; Gaps THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLOGSSG 59	k/DDBJ da BOED7754	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TRANSPOSON-TN21 HOMOLOGUE; TRANSPOSON-TN21 HOMOLOGUE; TRANSPOSON-TN21 HOMOLOGUE; Thibution of distinct microvariants of Tn5041 in environmental bacteria.";	subdivision; Pseudomonadaceae;	T; 124 AA. ted) sequence update) annotation update)

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80 THCEEASSLAEHKLQDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGGT 136

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Matches 54
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Matches 56
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01-NOV-1996
01-DEC-2001
                                                                                                  PRINTS; PR00040; HTHMERR, 1.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                  OSBORN A.M., Bruce K.D., Strike P., Ritchie D.A.; "Sequence Conservation between Regulatory Mercury from Mercury Polluted and Pristine Environments."; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ data-i-SIMILARITY: BELONGS TO THE MERR FAMILY OF TRAN
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EMBL; Z33484; CAA83892.1; -.
Interpro; IPR000551; HTH_Mer
Pfam; PF00376; merf; 1.
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"Sequence Conservation between Regulatory Mercury
from Mercury Polluted and Pristine Environments.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ data
-!- SIMILARTY: BELONGS TO THE MERR FAMILY OF TRAN
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Bacteria; Proteobacteria;
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                     Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 144 AA; 15832 MW; B71D7FF
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Pro; IPR000551; PF00376; merR;
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44 AA; 15652 MW; 1D6E1F50D37A1337
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94.78;
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96.68;
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TRANSCRIPTIONAL
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Q52395;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-P.stutzeri; STRAIN-OX; PLASMID-PPB; MEDLINE-86174347; PLAMEd-3007931; Brown N.L., Misra T.K., Winnie J.N., Schmidt A., Selff M., Silver "The nucleotide sequence of the mercuric resistance operons of pla "The nucleotide sequence of the mercuric for mer genes which R100 and transposon Tn501: further evidence for mer genes which enhance the activity of the mercuric ion detoxification system."; Mol. Gen. Genet. 202:143-151(1986).
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MEDLINE-85014891; PubMed-6091128;
Misra T.K. Brown N.L. Fritzinge
Haberstroh L., Silver S.;
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                                                                                                                          "Two aberrant mercury resistance stutzeri plasmid pPB."; Gene 208:37-42(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=P.stutzeri; STRAIN=OX; PMEDLINE=96105204; PubMed=8529897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kholodii G.Ya, Yurieva O.V., Lomovskaya O.L., Mindlin S.Z., Nikiforov V.G.; "Th5053, a mercury resistance transposon with J. Mol. Biol. 230:1103-1107(1993).
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SPECIES=P.stutzeri; STRAIN=OX; PI
MEDLINE=93253772; PubMed=8387603;
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Pseudomonas stutzeri (Pseudomonas perfectomarina).
Plasmid pWWO, and Plasmid pPB.
Bacteria; Proteobacteria; gamma subdivision; Pseud
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                                                                                                                                                                                                                                                                                                                                                                "Cloning and comparison of mercury- and o
determinants from a Pseudomonas stutzeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mercuric ion-resistance operons of plasmid R100 and transposon Tn501:
                        REGULATORS.
L; AJ344068; CAC86844.1;
L; U90263; AAC38229.1; -.
                                                                                                  SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 20,
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TrEMBLrel. 20, Last annotation update)
protein (Organomercurial resistance r
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gamma subdivision;
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tzeri plasmid.";
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RESULT 6
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Best Local
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PRINTS; PR00040; HTHMERR.
SMART; SM0042; HTH_MERR; 1.
SMSTE; PS00552; HTH_MERR_FAMILY; 1.
PROSITE; PS00552; HTH_MERR_TAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; Ts0564;
NA 18826 MW; 897D139E7BC182A9 CRC64;
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Plasmid; DNA-binding; Transcription regulation.
Plasmid; DNA-binding; Ts0560BEC88602FC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mikro.
Shigella flexneri.
Plasmid virulence plasmid pWR501.
Plasmid virulence plasmid pWR501.
                                              01-MAY-2000 (TREMBLIGE: 13, 01-MAY-2000 (TREMBLIGE: 13, 01-JUN-2001 (TREMBLIGE: 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                          MERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=21189246; PubMed=11292750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In501 repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AFK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AFK4
Plasmid group 5 plasmid
                                                                                       Q9R9W9;
                                                                                                    Q9R9W9
                                                                                                                                                                                                                                                                                                                                InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                         EMBL; AF348706; AAK18578.1;
                                                                                                                                                                                                                                                                                                                                                                                                        Shigella flexneri
                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERR
           Pseudomonas putida
                                   MerR (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete DNA sequence and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                           Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J.,
                                                                                                                                                                 108 THCEEASSLAEHKLKDVREKMADLARMEAVLSELVCACHARRGNVSCPLIASLQGGA
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                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                         2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSS 58
                                                                                                                                                                                                                                                                                                                                                                            ect. Immun. 69:3271-3285(2001).
SIMILARITY: BELONGS TO THE MER
                                                                                                                                                                                                                                                                                                                                                                      REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THCEEASSLAEHKLKDVREKMADLARMEAVLSDLVCACHARKGNVSCPLIASLQGKKEPR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00376; merR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 54; Conserv
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                           45.0%;
93.0%;
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Last annotation update)
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                                              Last sequence update)
Last annotation update)
                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 276; DB 2;
Pred. No. 1.4e-19;
2; Mismatches 8;
                                                                                                                                                                                                                             Score 276;
Pred. No. 1
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                  MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                  Mismatches
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                                                                                                   110
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                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 144;
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                                                                                                   B
                                                                                                                                                                                                                               ,6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                    large virulence plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae;
                                                                                                                                                                                                                                        Length 172;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q60233 PRELIMINARY; PRT; 144 AA.
Q60233 P75015; Q44314; Q51768; Q51808; Q52601; Q56390; Q56443;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bruce K.D., Lilley A.K., Bailey M.J.;
"mer sequences on plasmids.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
EMBL; AF092070; AAD52776.1; -.
InterPro; IPR000551; HTH_MerR.
"Four genes, two ends, and a res region are involved in transposition of fn5053: a paradigm for a novel family of transposons carrying either a mer operon or an integron."; Mol. Microbiol. 17:1189-1200(1995).
                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas sp. (strain ADP).
Plasmid pMER327, Plasmid RP1, and Plasmid pADP-1.
Bacteria; Proteobacteria; beta subdivision; Alcal
                                                                                                                                             SPECIES=C.testosteroni; STRAIN=SE3; Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                  "The sequence of the mer operon of pMER327/419 and transposon ends of pMER327/419, 330 and 05."; Gene 146:73-78(1994).
                                                                                                                                                                                                                                                                                          SPECIES=Alcaligenes sp., and P.fluorescens; TRANSPOSON=TN5053; MEDLINE=94341572; PubMed=8063107;
                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comamonas testosteroni (Pseudomonas testosteroni)
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Pseudomonas fluorescens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MERR
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NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                        Nikiforov V.G.;
                                                                       Kholodii G.Y., Mindlin S.Z., Bass I.A.,
                                                                                   MEDLINE=96130850; PubMed=8594337;
                                                                                                    SPECIES-unidentified;
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              Hobman
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=512, 294, 285, 32644, 338,
                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                      xanthomonas, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercuric resistance operon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00422; HTH_MERR; 1.
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                                                                                                                                                                                                                                                                            ., Kholodii G.,
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110 AA;
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12211 MW;
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                                                                                                                                                                                                                                                                              Nikiforov V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Last sequence update)
, Last annotation update)
regulatory protein (MERR protein).
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Pred. No. 2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                              Ritchie D.A.,
                                                                                                                                                                                                                                                                                                                                                      47660
                                                                       Yurieva O.V., Minakhina S.V.,
                                                                                                                                                                                                                                                                                                                                                                                 Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 110;
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RESULT 957492
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RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT 
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Best Local S
Matches 53
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EMBL; L20693; AAB05979.1; ...
EMBL; L23095; CAA80641.1; ...
EMBL; L23094; CAA80640.1; ...
EMBL; L23094; CAA80640.1; ...
EMBL; L40585; AAA98322.1; ...
EMBL; L40585; AAA9832.1; ...
EMBL; L33481; CAA83889.1; ...
EMBL; U66917; AAK50289.1; ...
InterPro; IPRO00551; HTH_Merr.
Dfam: DE00376. MGCE.1
                                                                                                                                                                                                                                                                                                                                                                           057492

957492;

01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001)
  Osborn A.M.;
                           STRAIN-SE31
                                                 SEQUENCE FROM N.A.
                                                                                          Osborn A.M., Bruce K.D., Submitted (DEC-1994) to
                                                                                                                                              STRAIN-SO1
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                         Enterobacter cloacae,
                                                                                                                                                                                                                                                                                                                                         MERR.
                                                                                                                                                                                                                                                                                                                                                          Regulatory protein.
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SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

Activator; DNA-blnding; Mercuric resistance; Mercury; Plasmid; Repressor; Transcription regulation.

SEQUENCE 144 AA; 16060 MW; E4B3EFEECA317F2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Xanthomonas; PLASMID-RPI; TRANSPO
MEDLINE-93253772; PubMed-8387603;
Kholodii G.Ya., Yurieva O.V., Lomovskaya
Mindlin S.Z., Nikiforov V.G.;
"Tn5053, a mercury resistance transposon
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [4]
SEQUENCE FROM N.A.
SPECIES-unidentified;
Kholodii G.Y.;
                                                                                                                                                                                                                   NCBI_TaxID=550,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEEA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 82.8
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a mercury resistance transposon with integron's ends.";
Biol. 230:1103-1107(1993).
                                                                                                                                                                                                                   571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASMID=RPI; TRANSPOSON=TN5053;
                                                                                                                                                                                                                                                                                                              and
                                                                                   Strike P., Ritchie D.A.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 2.7e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                             subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; ]
2.7e-19;
hes 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorlenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 144;
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Best Local 9
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007304;
01-JUL-1997
01-NOV-1999
01-JUN-2001
                                                   PRINTS; PRO0040; HTHMERR.

MERR; 1.

PROSTITE; PS00552; HTH_MERR, FAMILY; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription 17CC8F1005A33FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Yurieva O., Kholodii G., Minakhin L., Go
Mindlin S., Nikiforov V.;
"Intercontinental spread of promiscuous
in environmental bacteria.";
Mol. Microbiol. 24:321-329(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
DNA-binding; Transcription 238460FCE51754AD CRC64;
                                                                                                                            EMBL; Y09210; CAA70409.2; -.

EMBL; Y18976; CAB81570.1; -.

InterPro; IPB000551; HTH_MerR.

Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                  Russ.
                                                                                                                                                                                                                                                     Kholodii G.Y., Mindlin S.Z.,
                                                                                                                                                                                                                                                                                                   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                 Kholodii G.;
                                                                                                                                                                                                                                                                                                                              STRAIN-TC97;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-TC97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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EMBL; Z33485; CAA83893.1; -.
Interpro; IPRO00551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                Russ. J. Genet. 36:365-3
                                                                                                                                                                                                  "Molecular genetic analysis of the Tn5041 transposition system."; Russ. J. Genet. 36:365-373(2000).
-i-SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                              Nikiforov V.;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97303088; PubMed=9159519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MERR protein (Mercuric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 L-AASARGSH 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 THCEEASGLAEHKLKDVREKMADLARMEAVLSELVCACHARKGNVSCPLIASLQ--DGTK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                       REGULATORS
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 Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 81., 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 04, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
              44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance operon regulatory protein).
Pred. No. 6.24
1; Mismatches
             Score 269.5; DB 2
Pred. No. 6.2e-19;
                                                                                                                                                                                                                                                      Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 269.5; DB 2;
Pred. No. 6.2e-19;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                  mercury-resistance transposons
                             DB 2; Length 151;
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Q57106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-Acinetobacter sp.; STRAIN-BW3; PLASMID-PKLH207; TRANSPOSON-TNPKLH207 TNPKLH2-LIKE ABERRANT TRANSPOSON; Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CH210; TRANSPOSON-TN5059;
MEDLINE-9730308B; PubMed-919519;
Yurieva O., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E.,
Mindlin S., Nikiforov V.;
"Intercontinental spread of promiscuous mercury-resistance transposons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     057106; 008282; 008130; 008287; 008166; 008288; 008185; 01-NOV-1996 (TIEMHILFE). 01, Created) 01-NOV-1996 (TIEMHILFE). 01, Last sequence update) 01-DEC-2001 (TIEMHILFE). 19, Last annotation update) Regulatory protein (Mercury resistance operon regulatory protein) (MER
                                                                                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dissemination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osborn A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SE12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter sp., and Acinetobacter sp. LS56-7.
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Enterobacter cloacae,
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPOSON=TNPKLH204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Acinetobacter sp. LS56-7; PLASMID=PKLH204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osborn A.M., Bruce K.D., Strike P., Ritchie D. Submitted (DEC-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acinetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                       Kholodii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "pKLH2-like aberrant transposons and possible mechanisms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in environmental bacteria."
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                                                                                                      709026; CAA70240.1; -...

708993; CAA70195.1; -...

733483; CAA83891.1; -...

733482; CAA83890.1; -...

708992; CAA70185.1; -...

709025; CAA70237.1; -...
                                                                                                                                                                                                                                                                           REGULATORS.
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                                                   AJ245842; CAC80722.1; -. AJ250860; CAC38823.1; -.
                         IPR000551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OCT-1999) to the EMBL/GenBank/DDBJ databases
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                         HTH_MerR
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Best Local :
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01-JUL-1997
01-JUN-2001
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01-MAY-2000
01-JUN-2001
                                                                                     Pseudomonas sp., and Pseudomonas sp. ED23-33. Plasmid pMR26. Bacteria; Proteobacteria.
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Q9R9X0;
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SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Plasmid; Transcription regulation.

DNA-binding; Plasmid; Transcription regulation.

SEQUENCE 151 AA; 16529 MW; 239350FCE51754AD CRC64;
SPECIES=Pseudomonas sp.; STRAIN=K-62; PLASMID=PMR26;
                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruce K.D., Lilley A.K., Bailey M.J.;
"mer sequences on plasmids.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092069; AAD52705.1; -.
InterPro; IPR000551; HTH_MerR.
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                                                                                                                                                                                                Mercuric resistance operon
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Bacteria; Proteobacteria;
                                                                 NCBI_TaxID=306,
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STRAIN=KT2440;
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96.3%;
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81.4%;
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                                                                                                                                                                                                regulatory protein (MERR1
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No. 6.3e-19;
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Best Local :
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"Nucleotide sequence and expression of the organomercurial-resistance determinants from a Pseudomonas K-62 plasmid pMR26.";
Gene 189:151-157(1997).
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                                                                                                                                                                                                                                                                                                                                             MEDLINE-85155497; PubMed-6099319; Ogawa H.I., Tolle C.L., Summers A.O.; "Physical and genetic map of the organomercury resistance (Omr) inorganic mercury resistance (Hgr) loci of the IncM plasmid R83 Gene 32:311-320(1984).
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; Tanscription regulation.
SEQUENCE 144 AA; 15651 MW; AE25F7DF733A6734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas sp. K-62,
Pseudomonas sp. ED23-33, and
Rhizoblum meliloti (Sinorhizoblum meliloti)
Plasmid R831b, Plasmid pMR26, and Plasmid p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D83080; BAA20334.1; -.
EMBL; Y17897; CAC14697.1; -.
InterPro; IPRO00551; HTH_Merr.
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                                               SPECIES-E.coli;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                             Submitted (DEC-1996)
                                                                                                                                                                                                                               SPECIES=E.coli;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transposons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGAST 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEEASS
                                                                                                                                                                                                    <u>.</u>
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54; Conservative
                                                                                                                                                                                                Totis P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76885,
                                                                                                                                                                                                    Summers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.7%;
A.L.,
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                                                                                                                                                             the
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5; Mismatches
       Summers A.O.;
                                                                                                                                                                                                    A.O.;
                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 144; .2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pSB102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorlenko Z.H.,
                                                                                                                                                                                                                                                                                                                                                                                         Omr) and R831b."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 14
Q44191
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                              Q44191 PRELIMINARY;
Q44191;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mercury resistance plasmid pSB102 isolated from a microbial porcesiding in the rhizosphere of alfalfa."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM NO...

SPECIES-R. meliloti; PLASMID-PSB102;

TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718;

TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718;

TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Pseudomonas sp. Minakhin S., Minakhin
                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U77087; AAB49638.1; -. EMBL; AB013925; BAA36431.1; -. EMBL; Y17897; CAC14703.1; -. EMBL; AJ304453; CAC79199.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the two mer operons from a Peudomonas K-62 plasmid pMR26.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=Pseudomonas
Kiyono M., Hou H.P.;
                                              STRAIN-T217;
                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                       Agrobacterium tumefaciens.
                                                                                                                                                       MERR
                                                                                                                                                                   Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prosite; ps00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
sequence 144 AA; 15623 MW; 9DF4ED0B8A57D75D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000551; HTH_MerR
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidemic dissemination of Tn21-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
from Mercury Polluted and Pristine Environments.";
                            Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.;
                                                          SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=358;
                                                                                                          Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selbitschka W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular inventory of transposons from environmental bacteria: epidemic dissemination of Tn21-, Tn5041-, and Tn5053-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genetic organization and evolution of the bromercury resistance plasmid pSB102 isolated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turieva O., Nikiforov V.;
               Sequence Conservation between Regulatory Mercury Resistance Genes
                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                     62 CEEASS 67
                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                   2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATORS
                                                                                                                                                                                                                                                                                                                          LAGAST 143
                                                                                                                                                                                                                                                                                                                                                                                  THCEEASSLAEHKLQDVREKMADLARMEAVLSDLVCACHSRQGNVSCPLIASLQG--GTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                          Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ED23-33; TRANSPOSON=TN5058; Kholodii G., Mindlin S.,
                                                                                                                        alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 268; DB 2;
Pred. No. 8.2e-19;
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microbial population
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RESULT 15
Q99093
ID 99909
AC 99909
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DT 01-M
OS ACIN
OS ACIN
OG Plas
OG Plas
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RR E (3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-A.calcoaceticus; PLASMID-PKLH2;
MEDLINE-94134837; PubMed-8302940;
Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
Yurieva O.V., Nikiforov V.G.;
"Molecular characterization of an aberrant mercury resistance transposable element from an environmental Acinetobacter strain.";
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SPECIES-A.lwoffii; PLASMID-PKLH103, PKLH102, AND PKLH104;
Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,
Yurieva O.V., Nikiforov V.G.;
"PKLH1-like aberrant mercury resistance transposons of environmental Acinetobacter strains: spread, polymorphism and possible origin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                  "The shuffling function of resolvases.";
Gene 269:121-130(2001).
-i- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099093, PRELIMINARY; PRT; 151 AA. 099093; Ol-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                          SPECIES=Acinetobacter sp.; STRAIN=ED45-25; PLASMID=PKLH205; MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=A.calcoaceticus; PLASMID=PKLH2; Lomovskaya O.L., Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16591 MW; 548460FCE50240FC CRC64;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter sp. Plasmid pKLH2, Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid 30:303-308(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetika
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter calcoaceticus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mer operon regulatory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000551; HTH_Merr.
Pfam; PF00376; merr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 L-AASARGSH 146
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      REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pKLH103, Plasmid pKLH102, Plasmid pKLH104, and
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Pred. No. 1.2e-18;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
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             Search completed: May 28,
                                                                                                                                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                               EMBL; AF213017; AAA19678.1; -
EMBL; AJZ51539; CAB65953.1; -
EMBL; AJZ51517; CAB65939.1; -
EMBL; AJZ51009; CAB65945.1; -
EMBL; AJZ51009; CAB65949.1; -
EMBL; AJZ51706; CAB65949.1; -
EMBL; AJZ51706; CAB65949.1; -
InterPro; IPRO00551; HTH_Merr.
Pfam; PF00376; merr; 1.
time : 34 secs
                                                                                                                                                                                                PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PSO0552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; T49350FCE50240FC CRC64;
                                                   138 L-AASARGSH 146
                                                                                                62 CEEASSLAEH 71
                                                                                                                                                    Local Similarity es 56; Conserv
                                                                                                                                                    Conservative
                                                                                                                                                               43.5%;
              2003, 10:28:52
                                                                                                                                                   2;
                                                                                                                                                             Score 266.5; DB 2;
Pred. No. 1.2e-18;
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                                                                                                                                                   1.2e-18;
nes 9;
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Maximum DB
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     seq length: 0
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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613
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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 US-09-134-001C-2982
US-09-188-930-332
US-09-188-930-192
US-08-685-576-4
US-09-095-443-2
US-08-416-581B-1
US-08-416-581B-5
US-08-416-581B-9
US-08-852-091-12
US-08-852-091-12
US-08-956-652-12
US-08-956-652-12
US-08-956-652-12
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US-09-012-710-8
US-09-012-710-8
US-09-14-970-3
US-09-364-970-3
US-09-364-970-3
US-09-56-633A-12
US-09-556-273-8
US-09-556-1742-2
PCT-US95-17025-12
US-08-781-880-14
US-08-781-880-14
US-08-781-880-14
US-08-0058-489-35
US-09-058-6455-2
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Sequence 4, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 9, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appli
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Sequence
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Sequence 332, App
Sequence 192, App
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RESULT 2 US-09-188-930-332 ; Sequence 332, Application US/09188930A ; Patent No. 6150502 ; GENERAL INFORMATION: ; APPLICANT: Watson, James D. ; APPLICANT: Strachan, Lorna ; APPLICANT: Strachan, Lorna ; APPLICANT: Steeman, Matthew ; APPLICANT: Onrust, Rene ; APPLICANT: Onrust, Rene ; APPLICANT: Muxison, James Greg	Qy 50LIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKON 103  Db 64 SLKEIHLLFGVVDQDGERCKDMYAFTVQKTKEIERKVQDLLRIQRLLEELKEKCPDEKAI 123  Qy 104 VSCP 107  II  Db 124 YTCP 127	ע	RESULT 1  US-09-134-001C-2982  Sequence 2982, Application US/09134001C  Patent No. 6380370  GENERAL INFORMATION:  APPLICANT: Lynn Doucette-Stamm et al  PITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  FILE REFERENCE: GTC-007  CURRENT FILING DATE: 1998-08-13  PRIOR APPLICATION NUMBER: US/09/134,001C  CURRENT FILING DATE: 1997-11-08  PRIOR APPLICATION NUMBER: US 60/064,964  PRIOR APPLICATION NUMBER: US 60/055,779  PRIOR FILING DATE: 1997-08-14  NUMBER OF SEQ ID NOS: 5674  SEQ ID NO 2982  LENGTH: 138  TYPE: PRT  ORGANISM: Staphylococcus epidermidis  US-09-134-001C-2982	28 68.5 11.2 955 2 US-08-428-414A-3 Sequence 3, Appli 30 68.5 11.2 955 5 PCT-US94-00324-1 Sequence 1, Appli 31 66.5 10.8 425 1 US-08-938-105-3 Sequence 5, Appli 32 66.5 10.8 425 3 US-09-020-684-5 Sequence 5, Appli 34 66.5 10.8 425 3 US-09-020-684-5 Sequence 5, Appli 35 66.5 10.8 425 3 US-09-020-683-5 Sequence 5, Appli 36 66.5 10.8 425 4 US-09-020-683-5 Sequence 5, Appli 36 66.5 10.8 574 1 US-08-049-473-2 Sequence 5, Appli 38 66.5 10.8 574 1 US-08-049-473-2 Sequence 2, Appli 40 66.5 10.8 574 2 US-07-728-215-29 Sequence 2, Appli 66.5 10.8 574 2 US-07-728-215-29 Sequence 2, Appli 66.5 10.8 574 2 US-07-728-215-29 Sequence 2, Appli 66.5 10.8 573 2 US-08-338-085A-29 Sequence 2, Appli 66.5 10.8 573 4 US-08-938-085A-29 Sequence 2, Appli 66.5 10.7 386 2 US-08-559-303B-75 Sequence 2, Appli 65.5 10.7 386 2 US-08-559-303B-75 Sequence 2, Appli 65.5 10.7 386 2 US-08-559-303B-75 Sequence 7, Appli 65.5 10.7 659 3 US-08-820-170A-34 Sequence 77, Appli 65.5 10.7 810 2 US-08-820-170A-34 Sequence 34, Appli 65.5 10.7 810 2 US-08-820-170A-34
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TITLE OF INVENTION: Compositions Isolated From Skin Cells

APPLICANT:

Nakano, Takeshi

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RESULT 4
US-08-685-576-4
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; LOCATION: (239)..
US-09-188-930-192
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                                              Sequence 4,
Patent No. !
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 332
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                     Query Match
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SOFTWARE: FastSEQ for
SEQ ID NO 192
LENGTH: 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1
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                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: mouse
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 APPLICANT:
                APPLICANT:
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5. 6150502
                                                             Application US/08685576
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Kaibuchi,
Iwamatsu,
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27.58;
Akihiro
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Pred. No. 0.38;
5; Mismatches
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                                                                                                                                                      Sequence 2, Application Patent No. 6342593
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                 APPLICANT: Plowman, Gregory
APPLICANT: Peles, Eior
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8
FILING DATE: 05-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                      NUMBER OF SEQUENCES:
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APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
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TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
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                                                                                                                                                                                                                                                                                                                   34
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   STREET:
                  STREET:
                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                   ELEIKEMMARHKQELTEKDATIASLEETNRTLTSDVANLANEKEELNNKLKDVQEQLSRL 1006
                                                                                                                                                                                                                                                                                                                   EL----VCACHARKGNVSCPLIASLQGSSGTHCEEASSLA----EHKLKDVREKMADL 83
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E: Lyon & Lyon
633 West Fifth Street
Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%;
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1388;
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COUNTRY:

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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino acids
                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08369796 Patent No. 5716622
                                                             APPLICANT: James L. ....
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ANDRESSEE: Klauber & Jackson
ANDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEV 101 ...
CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/09/095,443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GQAGAISITS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 CHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACH 98
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 ALSVRPDTVRNLVQSMQVLSGVFTD-----VEASLKDIRDLLEEDELLEQKFQEAV---- 115
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les 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: IBM P.C. DOS 5.0 FastSEQ for Windows 2.0
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                                                                      APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
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                                            INFORMATION FOR SEQ
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT: Akira, Shizuo
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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770 amino acids
                                        (202)293-7860
OR SEQ ID NO: 1:
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TYPE:

amino acid

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RESULT 8
US-08-416-581B-5
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Patent No. 5719042
GENERAL INFORMATION:
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                                                                                                                                                  Matches
                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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APPLICANT: Akira, Shizuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCIWEESRLLQTAATAAQQ 125
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                                     56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
                                                                        73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                               5 EEASSLAEHKLKDVR------EKMADLARMETVLSELVCACHARKGN-VSCPLIASLQ 55
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                  Linear
                                                                                                                                                                                                                                              protein
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                                                                                                                                                                    11.5%; Score 70.5; DB 1; Length 770; 23.3%; Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/416,581B
                                                                                                                                                  20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Q-37891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                    38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 21;
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RESULT 9
US-08-416-581B-9
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                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                         Sequence 12, Appli
Patent No. 5883228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kishimoto, Tadamitsu
APPLICANT: AKira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 04-APR-19
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                       TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
                                                                                                                                                APPLICANT: James E. Darnell, Jr
APPLICANT: Zilong Wen
                                   CORRESPONDENCE ADDRESS:
                                                         NUMBER OF SEQUENCES:
                                                                                                            APPLICANT: Curt M. Hory APPLICANT: Zhong Zhong
                                                                                                                                                                                                                                                                                                                          126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                   73 QESNYLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 6-65825/1994 FILING DATE: 04-APR-1994
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                                                                                                                                                                                                                                                                                                                                                               56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
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STREET:
                 ADDRESSEE:
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411 Hackensack Avenue
                                                                                                                                Zilong Wen
Curt M. Horvath
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                   Klauber & Jackson
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Pred. No. 9.2;
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CITY: Hackensack

New Jersey

COUNTRY:

USA

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APPLICANT: Darnel
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        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/820,754
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEI TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
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FILING DATE:
                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                  CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                      07601
                                                                                                                                                                                                            New Jersey
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19-MAR-1997
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06-JAN-1995
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                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECEPTOR RECUGNALIZATION TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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APPLICANT:
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TELEPHONE: 201 487-5800
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ATTORNEY/AGENT INFORMATION:
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                     FILING DATE:
                                     APPLICATION NUMBER:
                                                                                                                                                                        ZIP: 07601
                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                               CITY: Hackensack
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APPLICATION NUMBER: US 07/980,498
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
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                                     US/08/956,652
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APPLICATION NUMBER: 0

FILING DATE:

APPLICATION NUMBER:

11-MAR-1994

US 08/212,185

US 07/980,498

08/212,185

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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICATION NUMBER: US 08
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07
FILING DATE: 19-MAR-1992
                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, TITLE OF INVENTION: SEQUENCES AND METHODS OF USE 1 NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                           STREET: 411 Hacke
CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                  CLASSIFICATION:
                                      FILING DATE:
                                                                                                                                                                                 COUNTRY: UZIP: 07601
                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 EEASSLAEHKLKDVR------EKMADLARMETVLSELVCACHARKGN-VSCPLIASLQ 55
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                                                                                                                                                                                                                New Jersey
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411 Hackensack Avenue
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Schindler, Christian W.
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                                                                                                                                        Floppy disk
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                                                       us/08/956,869
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Pred. No. 9.2;
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US-08-956-869-12
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 770 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201
TELEFAX: 133521
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                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                             CITY:
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                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 EEASSLAEHKLKDVR-----EKMADLARMETVLSELVCACHARKGN-VSCPLIASIQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                             411 Hackensack Avenue, 4th Floor
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Kuriyan, John
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24-SEP-1993
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                                                                                                                                                              Release #1.0, Version #1.30
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                                                                                                                              US/09/012,710
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                    600-1-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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TELEPHONE: 201-40.

201-487-5800

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US-08-948-547-12
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      PILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: WO US93/02569
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
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Patent No. 6
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
ADDRESSED: FACTORS:
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
FILING DATE:
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HYPOTHETICAL:
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                                                                                                                                                                                                  APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 ....
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
  REFERENCE/DOCKET NUMBER:
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STRANDEDNESS: sin
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al Similarity 23.3%; Pred. No. 9.2;
24; Conservative 20; Mismatches 38; Indels 21; Gaps
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600-1-073 CIP
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-547-12
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                                                                                                                                                                        Matches
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
                                        56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
                                                                           73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 201 343-1684
                                                                                                                                                             Local Similarity 23.3%; Pred. No. 9.2; ses 24; Conservative 20; Mismatches
                                                                                                                    5 EEASSLAEHKLKDVR------EKMADLARMETVLSELVCACHARKGN-VSCPLIASLQ 55
                                                                                                                                                                                     11.5%; Score 70.5; DB 3; Length 770; 23.3%; Pred. No. 9.2;
                                                                                                                                                             38; Indels 21; Gaps
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Search completed: May 28, 2003, 10:29:38 Job time : 18 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                                                                                Published_Applications_AA: *
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SUMMARIES
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Sequence 12, Appl	Sequence 24, Appl	Sequence 305, App	Sequence 780, App	Sequence 56, Appl	Sequence 8, Appli	Sequence 116, App	Sequence 260, App	sequence /, Appli			12.	N.		Sequence 11, Appl		Sequence 22, Appl	sequence 332, App	Column to the total	Sequence 192 App	Sequence 458 App	Description		

US-09-866-050A-192
; Sequence 192, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:

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RESULT 2

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63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	64	64	64	64	64	64	64	64	64.5	65.5	65.5	65.5	66	66	66.5	69	69	69
10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.5	10.7	10.7	10.7	10.8	10.8	10.8	11.3	11.3	11.3
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US-10-092-390-2	US-10-028-392-5	US-09-796-753-124	US-09-796-753-100	US-10-092-390-4	US-09-866-050A-335	US-09-764-869-917	US-10-091-504-917	US-10-116-260-1	10-11	US-10-115-671-1	US-10-116-561-1	US-10-115-695-1	US-09-254-590-1	US-09-922-364A-1	US-09-738-626-5780	US-09-381-624A-3	US-10-011-064-5	US-09-976-165-34	US-09-753-143-75	US-09-842-758-18	US-09-864-761-44770	US-10-072-841-29	US-10-043-487-330	US-09-938-803-13	US-09-800-362-2
2	Sequence 5. Appli		_	Sequence 4, Appli	•	Sequence 917, App	91	ا ب	ا ت	μ.	<u>.                                    </u>	Sequence 1, Appli	۲.	Sequence 1, Appli	578		Sequence 5, Appli	Sequence 34, Appl		Sequence 18. Appl		Sequence 29, Appl	Sequence 330, App	13	Sequence 2, Appli

## FILE REFERENCE: 11000.1011c4U CURRENT APPLICATION NUMBER: US/09/866,050A CURRENT FILING DATE: 2001-05-24 NUMBER OF SEQ ID NOS: 725 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 458 LENGTH: 296 TYPE: PRT ORGANISM: Mouse RESULT 1 US-09-866-050A-458 Sequence 458, Application US/09866050A Publication No. US20030040471A1 GENERAL INFORMATION: US-09-866-050A-458 Matches Query Match Best Local Similarity APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene APPLICANT: Murison, James G. APPLICANT: Murison, James G. APPLICANT: Kumble, Krishanand D. TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods for Their Use 74 ---CACRNGGLCHAINGSCSCPLGWMGPHCE 101 38 ACDPVSGTCICP----PGKTGGHCERGCPODRFGKGCEHK---92 ELVCA-----CHARKGNVSCPSAWSHPQFE 116 38 ACHARKGNVSCPLIASLQGSSGTHCEEA-----SSLAEHKLKDVREKMADLARMETVLS 91 25; Conservative 14.4%; Score 88.5; DB 9; Length 296; 27.5%; Pred. No. 0.23; ative 2; Mismatches 25; Indels 3 Indels 39;

Gaps

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; Sequence 22, Application US/10259042
; Publication No. US20030077644A1
                                   RESULT 4
US-10-259-042-22
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LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
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LENGTH: 299
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CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
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TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Strach
APPLICANT: Sleema
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APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Mouse
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                                                                                                                 77 --- CACRNGGLCHATNGSCSCPLGWMGPHCE 104
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                                                                                                                                                                                                                                                                                      Local Similarity
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Sleeman, Matthew
Onrust, Rene
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Sleeman, Matthew
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27.58;
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Pred. No. 0.23;
2; Mismatches 25; Indels 3
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LENGTH: 337
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION. Diagnosis and Treatment of Diseases Caused by Mutations in CD7
FILE REFERENCE: SAG 0105 PUS
CURRENT APPLICATION NUMBER: US/10/259,042
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                           PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 SLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAW 110
                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                                                                                         APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/234,687
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Hanzel, David K.
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Pred. No. 14;
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οy
                                                                                                                                                                ; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-994-11
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CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/790,621
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: PCT/US00/23663
PRIOR FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: US 60/151,348
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 36
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                                                                               Matches
                                                                                                                        Query Match
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                                                                                                                                                                                                                                                           SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/10084994
Publication No. US20030023070A1
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OTHER INFORMATION: EXPRESSED IN
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OTHER INFORMATION: EXPRESSED IN
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TITLE OF INVENTION: Attractin-Like Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT011P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 34088
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AP000215.1
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38 ACHARKGNVSCPLIASLOGSSGTHCEEA---SSLAEHKLKDVREKMADLARMETVLSELV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 -----SHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 QKHCEALR-----REK-----EVSATLKSTVEALHTQKRELRCSLEREREKPAWL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 QAELEQSHPRLKE 196
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSC-----PSAW- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 CVHQDTQAHHALLQKLKEEKSRVVDLQAMLEKVQQQ----ALHSQQ-----QLEAEA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CEEASSLAEH----KLKDVREKMADL-ARMETVLSELVCACHARKGNVSCPLIASLQGSS 58
                                                                          24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.2 INFORMATION: EST_HUMAN HIT: BF375387.1, EVALUE 2.00e-37 INFORMATION: SWISSPROT HIT: O95613, EVALUE 1.00e-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                               11.6%;
26.7%;
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                                                                        8; Mismatches
                                                                                            Score 71; DB
Pred. No. 23;
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IN BT474, SIGNAL = 7.4
IN BONE MARROW, SIGNAL =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN LUNG, SIGNAL = 10
IN HELA, SIGNAL = 13
IN ADULT LIVER, SIGNAL = 10
IN BRAIN, SIGNAL = 9.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN HEART, SIGNAL = 6.8
IN HBL100, SIGNAL = 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71; DB 10; Length 245; Pred. No. 11;
                                                                                                               DB 9; Length 474;
                                                                     24;
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                                                                     Indels
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                                                                 34; Gaps
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// OTHER INFORMATION: Description of Artificial Sequence: ALP
// OTHER INFORMATION: polypeptide sequence
US-10-020-215-2
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; Publication No. US20030008347A1
; GENERAL INFORMATION:
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  Query Match
Best Local Similarity
                                                                                                                                                                                                                                          SEQ ID NO 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/020,215
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/095,443
PRIOR FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09884001 Publication No. US20020182656A1
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PLOWMAN, GREGORY
APPLICANT: PELES, EIOR
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS
FILE REFERENCE: 038602/1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Virca, G. Duke
APPLICANT: Willis, Cynthia R.
APPLICANT: Willis, Cynthia R.
TITLE OF INVENTION: Methods for Regulating Vascularization Using GEF
TITLE OF INVENTION: Containing NEK-Like Kinase (GNK)
FILE REFERENCE: Immunex GNK/SGNK PCT
CURRENT APPLICATION NUMBER: US/90/884,001
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/113,003
PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/049,477
PRIOR FILING DATE: 1997-06-11
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10
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APPLICANT: Peschon, Jacque
APPLICANT: Sims, John E.
                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                             FEATURE:
                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                 LENGTH: 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 KELSAQMELLRQEVKEKEADFLAQEAQLLEELEASHITEQQLRASLWAQEAKAAQLQLRL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 RSTESQLEALAAEQQPGNQAQAQQLASLYSALQQALGSVCESRPELSGGGDSAPSVW 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 EEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPL-----IASLQ-GS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 C-----ACHARKGNVSCPSAWSHPQFEK 117
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Virca, G. Duke
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    11.6%;
24.6%;
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  Score 71;
Pred. No.
DB 9;
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                     Length 1274;
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APPLICANT: Doi, Masayuki
APPLICANT: Doi, Masayuki
APPLICANT: Thyboll, Jill
TITLE OF INVENTION: Recombinant Laminin 10
FILE REFERENCE: 99-274-F
CURRENT APPLICATION NUMBER: US/10/037,182
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,449
PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-12
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/10037182 Publication No. US20030044899A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12
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                                           SOFTWARE: PatentIn Ver. SEQ ID NO 10
                                                                                                                                                                                                               APPLICANT: Thyboll, Jill
TITLE OF INVENTION: Recombinant Laminin 10
FILE REFERENCE: 99-274-F
CURRENT APPLICATION NUMBER: US/10/037,182
CURRENT FILING DATE: 2001-12-21
                                                                       PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                           PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/279,282
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tryggvason, Karl APPLICANT: Doi, Masayuki
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1443 IKQIRNFLTEDSADLDSIEAVANEVL-----KSGNASTP-------QQLQNLTE 1484
                         ENGTH: 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ARKGNVSCPS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 LKDVR----EKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEEASSLAE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 11.6%; Score 71; DB 9; Length 1725; Local Similarity 25.6%; Pred. No. 1.1e+02; Local Similarity 18; Mismatches 17; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 HKLKDVREKMADLARMETVLSE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 EASSL-AEHKLKDVREKMADLARMETVLSELV-----CA 38
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; ORGANISM: Mus musculus US-10-037-182-10
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CURRENT APPLICATION NUMBER: US/09/938,275
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1786
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09938275 Patent No. US20020111309A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              Sequence 260, Application US/10082830 Publication No. US20030077604A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.6%; Score 71; DB 10; Length 1786; Best Local Similarity 25.6%; Pred. No. 1.2e+02; Matches 21; Conservative 18; Mismatches 17; Indels 2
                                                                                                                                                                                                                                                                   APPLICANT: Sun, APPLICANT: Recil APPLICANT: Salc APPLICANT: Liu,
SEQ ID NO 260
LENGTH: 2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: MUS MUSCULUS
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Swissprot P02469
DATABASE ENTRY DATE: 1989-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Therapeutic and Diagnostic Applications TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gerardo Castillo APPLICANT: Alan Snow.
                                                         CURRENT APPLICATION NUMBER: US/10/082,830 CURRENT FILING DATE: 2001-10-29 PRIOR APPLICATION NUMBER: 60/243,802 PRIOR FILING DATE: 2000-10-27 NUMBER OF SEQ ID NOS: 282
                                                                                                                                                                                APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0249
                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1546 ----DIRERVETLSQVEVILQQ 1563
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                                          PatentIn Ver.
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Salceda, Susana
                                                                                                                                                                                                                                                                           Liu, Chenghua
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US-09-796-753-116
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1132 RSTESQLEALAAEQQPGNQAQAQAQLASLYSALQQALGSVCESRPELSGGGDSAPSVW 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 SGTHCEEASSLAEHKLKDVREKMADLARMETVLSE-LVCACHARK----GNVSCPSAW 110
                                                                                                                      APPLICATION NUMBER: 09/
FILING DATE: 2000-03-01
APPLICATION NUMBER: 09/
FILING DATE: 2000-05-14
                         FILING DATE: 2000-06-22
APPLICATION NUMBER: 09/
FILING DATE: 2000-07-31
                                                                                                                                                                                                                APPLICATION NUMBER: 09/4
FILING DATE: 1999-12-29
APPLICATION NUMBER: 09/4
FILING DATE: 1999-12-29
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                                                            APPLICATION NUMBER: FILING DATE: 2000-0
                                                                                           APPLICATION NUMBER: FILING DATE: 2000-(
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                APPLICATION NUMBER:
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FILING DATE: 1999-07-30
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FILING DATE: 1998-12-30
APPLICATION NUMBER: 09//
FILING DATE: 1998-12-30
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FILING DATE: 1999-06-30
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VENTION: SECRETED PROTEINS AND USES THEREOF
NCE: 7853-227-999
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2000-06-29
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                                           09/630,334
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US-10-045-792-8
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SEQ ID NO 116
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PRIOR APPLICATION NUMBER: 09/6
PRIOR FILING DATE: 2000-09-30
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PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                         STRANDEDNESS: single
                                                                          LENGTH: 770 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/012,710 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/045,792 FILING DATE: 19-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 411 Hackensack Avenue, 4th Floor
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Darnell, Jr., James E.
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27.2%;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-10-045-792-8
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US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    문
                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56
Search completed: May 28, 2003, 10:38:14 Job time: 59 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein interactions in adipocyte cells
FILE REFERENCE: 84767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION UNMBER: US 60/259,377
PRIOR APPLICATION UNMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
LENGTH: 770
TYPE: PRI
ORGANIEM: Homo sapiens
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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## SUMMARIES

AUTHORS TITLE JOURNAL	SOURCE ORGANISM REFERENCE	AX473152 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	9		Δ.Δ. Δ. ω.		40 40	38	3 G		ωί			28		25	23 24	22		19	17 18			12			<b>9</b> 7		л⊪	ωΝ	_ : :	Result No.
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Metal binding proteins, recombinant host cells and methods
Patent: WO 0330962-A 17 18-APR-2002;
UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
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AX473150 435 bp Sequence 1 from Patent WO0230962.

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PAT 09-AUG-2002

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                                                                                                                                                                                      Direct Submission

Submitted (18-DEC-2001) Kholodii G.Y., Russian Academy of Sciences, Submitted of Molecular Genetics, Kurchatov Sq. 2, Moscow 123182,
                                                                                                                                                                                                                                                                                                               Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.Z. and Nikiforov,V.G. Distribution of distinct microvariants of Tn5041 in environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas fluorescens (strain KHP22) transposon Tn5041G, partial sequence (region of insertion of Tn21 homologue).
                                                                                                                                                                             Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  merR gene; MerR protein.
                                                                                                                                                                                                                                                           Kholodii,G.Y
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                                                                                                                                                                                                                                                                                                                                                                        Seudomonas
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                                                                                                                                                                          sequence Y09209
                         /country="Kyrgyzstan:Khaidarkan"
/note="isolated from mercury mine, ore"
                                                           /sex="Tra+ (narrow range)"
/plasmid="pKHP22"
transposon="In5041G"
                                                                                           /db_xref="taxon:294"
                                                                                                           /strain="KHP22"
                                                                                                                       organism="Pseudomonas fluorescens"
                                                                                                                                                       Location/Qualifiers
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/db_xref="taxon.623"
/note="77021 of Plasmid R100"
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Pred. No. 3.3e-26;
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                                                                                                                                                                        RUSSIA
                                                                                                                                                                                                   Submitted (18-DEC-2001) Kholodii G.Y.,
                                                                                                                                                                                                                                                                                                      Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.Z. and Nikiforov,V.G. Distribution of distinct microvariants of Th5041 in environmental
                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas fluorescens.
Pseudomonas fluorescens
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                                                                                                                                                                                     Institute of Molecular Genetics,
                                                                                                                                                                                                                                            Kholodii,G.Y
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/transl_table=11
/product="MerR protein"
/49 c 119 g 8
                                               /sex="Tra+ (narrow range)"
/plasmid="pKLH22"
          /country="Kyrgyzstan:Khaidarkan"
/note="isolated from mercury mine, ore"
                                                                                /db_xref="taxon:294"
                                                                                                      /strain="KHP25"
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/rpt_type=INVERTED
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/transposon="Tn21deltaIn2"
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                                                                                                                                                                                                                                                                          1 (bases 1 to 3763)
Barrineau, P., Gilbert, P., Jackson, W.J., Jones, C.S., Summers, A.O. and Wisdom, S.
Draft entry and sequence in computer readable form for [2] kindly provided by A.O.Summers, 15-SEP-1986. Potential Shine-Dalgarno sequences are located at positions 157- 162 (13.1 kd), 590-596 (12.4 kd), 1740-1745 (59 kd) and 545-542 (15.9 kd). A single 38 bp inverted repeat, which delimits the leftward end of Tn21, Tn4 and Tn501 extends from nucleotide 65-102. A promoter region for the
                                                                                                                                                                                                                                                                                                                                                                 merA gene; merR gene; merT gene; mercuric reductase. Plasmid NR1 (IncFII) from E.coli DNA, clone pDB7.
                                                                                                            Unpublished (1986)
[2] reviser (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid NR1 mercury resistance K03089
                                                                                                                                                  2 (bases 1 to 3763)
Summers, A.O.
                                                                                                                                                                                                                                     plasmid NR1
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/protein_id="CAD19592.1"
/protein_id="CAD19592.1"
/db_xref="GI:19848213"
/tanslation="vertireryQrkGLLPEPDKPYGSIRRYGEADVVRVKFVKSAQRLG
/translation="vertireryQrkGLLPEPDKPYGSIRRYGEADVVRVKFVKSAQRLG
FSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKG
NVSCPLIASLQGEAGLARSAMP"
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/transposon="Tn21deltaIn2"
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96.6%;
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Pred. No. 3.3e-26;
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structural genes is located between positions 366-585. This area contains regions of dyad symmetry which might function as operator sites for merR, which negatively regulates the expression of the structural genes as well as its own expression. The proteins deduced from the open reading frames all have counterparts in other organisms. The 12.4 kd and 15.0 kd predicted peptides are located in the inner membrane and have no detectable precursors. The 9.4 kd peptide is soluble, is processed to a 12 kd form and is for the most part associated with the periplasm. The first 30 bases were replaced with the corrected sequence from [2]. The rest of the revisions are in the sites table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="aab59072.1"
/protein_id="aab59072.1"
/db_xref="GI:455296"
/translation="menulemutigyfakaagynvetirfygrkgllrepdkpygsir
/tyanslation="menulemutigyfakaagynvetirfygrkgllrepdkpygsir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(98. .532)
/note="15.9 kd merR protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="magahefrohgfharqvghllahvlelvfgoaagllavgaivep
QQLGNLVQTEPOPLCRFHEFHPNHVRLPIAADAAVRLVRFPQQALALIEADCLHVDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /plasmid="Plasmid NR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRAKSAIFSRTSLSLCSARLLASSQWVPSSSRNSSAISSRLNPSRCADETNFTRTTSASP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAB59073.1"
/db_xref="GI:150391"
                                                                                                                                                /translation="MGLMTRIADKTGALGSVVSAMGCAACFPALASFGAAIGIGFLSQ
YEGLFISRLLPLFAALAFLANALGWFSHRQWLRSLLGMIGPAIVFAATVWLLGNWWTA
NLMYVGLALMIGVSIWDFVSPAHRRCGPDGCELPAKRL"
                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mkklfaslalaaavapvwaatqtvtlavpgmtcaacpitvkkal
skvegvtkvdvgfekreavvtfddtkasvqkltkatadagxpssvkq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:150393"
/translation="MSEPQNGRGALFAGGLAAILASTCCLGPLVLVALGFSGAWIGNL
TVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/protein_id="AAB59074.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLGKNANGQVFQIIFHIA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="13.1 kd protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAB59076.1"
/db_xref="GI:150394"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="6.5 kd protein"
/transl_table=11
/protein_id="AAB59078.1"
                                                                                                                                                                                                                                         /transl_table=11
/protein_id="AAB59077.1"
/db_xref="GI:150395"
                                                                                                                                                                                                                                                                                                                                                        /note="15.0 kd merTC protein"
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                                                                                            /note="Hg(II) reductase (59.0 kd merA)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases 849 to 2189)
Misra,T.K., Brown,N.L., Fritzinger,D.C., Pridmore,R.D.,
Barnes,W.M., Haberstroh,L. and Silver,S.
Mercuric ion-resistance operons of plasmid R100 and transposon
Tn501: the beginning of the operon including the regulatory rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohtsubo,H., Nyman,K., Doroszkiewicz,W. and Ohtsubo,E. Multiple copies of iso-insertion sequences of IS1 in Shigella dysenteriae chromosome
                                                                                                                                                                                                                                                                           Ohtsubo, H. and Ohtsubo, E. Nucleotide sequence of an insertion element, IS1 Proc. Natl. Acad. Sci. U.S.A. 75 (2), 615-619 (1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                               4 of
                                                                                                               6265806
                                                                                                                                             Nature 292 (5824), 640-643 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J01730.1 GI:151742
IS1 insertion sequence; merC gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid R100 putative (insA), putative (insB), merR (merR), putative (merT), merC (merC), mercuric reductase (merA), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /citation=[1]
/replace=""
596 a 1198 c 1189 g
117 bp upstream of EcoRII site.
                                                                                                                                                                                                                                                                                                                                                                     Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                reductase; transposon.
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                                                                                                                                                                                                                                (sites)
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LGSGAAMAAALKAVEQGARVTLIERGTIGGTCVNVGCVPSKIMIRAAHIAHLRRESP
FDGGIAATTPTIQRTALLAQQQARVDELHAKKEILEGRIDKTITVLHGSAAFKDNRNL
LVQLNDGGERVVAFDRCLIATGASPAVPIPGLKDTPYWTSTBALVSETIPKRLAVIG
SSVVALELAQAFARLGAKVIILARSTLFFREDPAIGEAVTAAFRMEGIEVREHTQASQ
VAYINGEGDGEFVLTTAHGELRADKLLVATGRANFUTRKLALDATGVTLTPQGAIVID
GMRTSVEHIYAAGOCTDQPQFVYVAAAAGTRAAINMTGGDAALNLTAMPAVVFTDPQV
ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
PEAGCLIGTAALAIRNMTVQELADQLFPYLTMVEGLKLAAQTFNKDVKQLSCCAG*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /replace=""
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/replace=""
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/translation="MSTLKITGMTCDSCAVHVKDALEKVPGVQSADVSYAKGSAKLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 164.4; DB 1; Length 3763; Pred. No. 2.9e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; merT gene; mercuric
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    regulatory region
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Three R100 derived small circular plasmids (pSM1, pSM2, pSM5) contain ISIR. pSM2 consists of map units 82.7-89.3 (the 3' end of ISIR) in circularized form. pSM1 is the same as pSM2, except for a deletion of map units 87.4-88.6. pSM1 is consists of map units 83.4-89.3 in circularized form.

Potential -35 regions are found at positions 980-984 and 1402-1406 and -10 regions at positions 999-1006 and 1425-1431. Unidentified reading frames are found at positions 2143-2565, 4688-4924 (gtg start codon), and 4921 to 5593. [4] noted two other ORF's in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence for [3], [5] and [4] kindly provided on tape by T.K.Misra ISI from [1] was renamed ISIR after [2] discovered that there are several ISI iso-insertion sequences. The 5 and 3' ends of ISIR are approximate inverted repeats. [2] found the CDS regions annotated below conserved among several ISIs. Deletion mutations in either of these two coding frames or in the two ends of ISIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              start codon), and 4921 to 5593. vicinity of the merR gene.
[2] sites; insA and insB spans.
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Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A., Lien, C., Sieff, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="
158..4
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                                                                                                                                                                                                                                  /note="putative"
                                                                                                                                                                                                                                                             /gene="insB"
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                                                                                                                                                                                                                                                                                                            'gene="insB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="putative"
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                                          Conservative
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SKYEGVSKYDVGFEKREAVVTFDDTKASVQKLTKATADAGYPSSVKQ"
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TVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
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/Translation-"MSTLKITGMTCDSCAVHVKDALEKVPGVOSADVSYAKGSAKLAI
/EVGTSEDALITAAVAGLGYRATLADAESVSTPGGLLDKMRDLLGRNDKTGSSGALHIAV
IGSGGAAMAALKAVEGOARVTLIERGTIGGTCVNYGCVPSKIMIRAAHIABLREESP
PDGGIAATTPTIORTALLAQQQARVDELRHAKYEGILEGNPAITTLHGSAREKDNRNI
IQQLANDGGERVVAFDRCLLATGASPAVPPIPGLEADTPYMFAFRALGETIPKEHTQASQ
SSVVALELAQARAHGAKYTILARGSPAVPPIPGLAVTGAFRWEGIEVREHTQASQ
VAYINGEGDGEFVLTTAHGELRADKLLVATGRAPNTRKLALDATGVTLTPQGAIVIDE
VAYINGEGDGEFVLTTAHGELRADKLLVATGRAPNTRKLALDATGVTLTPQGAIVIDE
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ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
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/transl_table=11
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                                                                                                                                                                                           AALQRLCFVRAAFEAGIGLDALARLCRALDAADGAQAAAQLAVVRQLVERRRAALAHL
                                                                                                                                                                                                               /trans1_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA92263.1"
/db_xref="GI:151752"
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/gene="merD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembled sequence of transposon Tn21 containing transposition genes, the integron In2, and the mercury resistance operon. AF071413
                                                                                                                                                                                                                                                                                                                                    Silver, S. Mercuric reductase structural genes from plasmid R100 and transposon Tn501: functional domains of the enzyme Gene 34 (2-3), 253-262 (1985) 85232071
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2 (bases 18411 to 19672)
Misra, T.K., Brown, N.L., Fritzinger, D.C., Pridmore, R.D.,
Barnes, W.M., Haberstroh, L. and Silver, S.
Mercuric ion resistance operons of plasmid R100 and transposon
Tn501: the beginning of the operon including the regulatory region
and the first two structural genes
and the first two structural genes
Proc. Natl. Acad. Sci. U.S.A. 81 (19), 5975-5979 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diver, W.P., Grinsted, J., Fritzinger, D.C., Brown, N.L., Altenbuchner, J., Rogowsky, P. and Schmitt, R. DNA sequences of and complementation by the tnpR genes of Tn21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
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J. Mol. App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Wisdom, S. The DNA sequence of the mercury resistance operon of the IncFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 15973 to 19672)
Barrineau, P., Gilbert, P., Jackson, W.J., Jones, C.S., Summers, A.O.
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                                                                        6 (bases 3057 to 4105)
Hyde, D.R. and Tu,C.P.
tnpM: a novel regulatory gene that enhances Tn21 transposition and suppresses cointegrate resolution
CCell 42 (2), 629-638 (1985)
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Misra,T.K., Brown,N.L., Haberstroh,L., Schmidt,A., Goddette,D.
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7 (bases 14935 to 15434)
Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A.,
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                                                                   Levesque,C., Brassard,S., Lapointe,J. and Roy,P.H. Diversity and relative strength of tandem promoters for the antibiotic-resistance genes of several integrons
                                                                                                                                                                                                                                                                                                                                      14 (bases 14967 to 15674)
Allmeier, H., Cresnar, B., Greck, M. and Schmitt, R.
Complete nucleotide sequence of Tn1721: gene organization and novel gene product with features of a chemotaxis protein Gene 111 (1), 11-20 (1992)
                                                           Gene 142 (1), 49-54 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mercier, J., Lachapelle, J., Couture, F., Lafond, M., Vezina, G. Boissinot, M. and Levesque, R.C. Structural and functional characterization of tnpI, a recompose in Tn21 and related beta-lactamase transposons J. Bacteriol. 172 (7), 3745-3757 (1990)
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Guerineau, F., Brooks, L. and Mullineaux, P.
Expression of the sulfonamide resistance gene from plasmid
Plasmid 23 (1), 35-41 (1990)
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A novel family of potentially mobile DNA elements encoding site specific gene-integration functions: integrons Mol. Microbiol. 3 (12), 1669-1683 (1989)
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The nucleotide sequence of the mercuric resistance operons of plasmid R100 and transposon Tn501: further evidence for mer genes which enhance the activity of the mercuric ion detoxification
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Ward, E. and Grinsted, J.
The nucleotide sequence of the tnpA gene of Tn21
Nucleic Acids Res. 15 (4), 1799-1806 (1987)
87146495
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                                                                                                                                          Direct Submission
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24 (bases 1 to 19672)
Liebert, C.A., Hall, R.M. and Summers, A.O.
Transposon Tn21, flagship of the floating genome
Mol. Biol. Rev. 63 (3), 507-522 (1999)
                                                                           Direct Submission
                                                                                                         GenBank Accession Number x12870 27 (bases 7540 to 14934)
                                                                                                                                                                             Sundstroem, L.
                                                                                                                                                                                         correction of sequence 26 (bases 4106 to 7539)
                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                          Partridge, S.R. and Hall, R.M. In34, a complex In5-like cla
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Binding of the purified integron DNA integrase Intl1 to integron-
and cassette-associated recombination sites
Mol. Microbiol. 29 (2), 477-490 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gravel, A., Fournier, B. and Roy, P.H. DNA complexes obtained with the integron integrase IntIl at the
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Recchia,G.D. and Hall,R.M.
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Characterisation of specific and secondary recombination sites
recognised by the integron DNA integrase
Nucleic Acids Res. 22 (11), 2071-2078 (1994)
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Brown, H.J., Brookes, D.E. and Stokes, H.W.
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Bacteriol. 176 (11), 3257-3268 (1994)
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                        51.2%;
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                      Score 164.4; DB 1
Pred. No. 2.7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-SEP-1999) National Chung Hsing University, Institute of Molecular Biology, 250 Kuo Kuang Road, Taichung, Taiwan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Chen, J.-H. and Chen, J.-Y.
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TnSF1, a Tn21-like transposon in Shigella flexneri
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                                                                                                                                                                                                         yahA; istA; istB; ybbA; sull; gacEdeltal; aadAl; intR; tniBdeltal; tnpA; ybjA; cat; insA; sull; gacEdeltal; aadAl; intR; tnpM; tnpR; tnpA; ybjA; cat; insA; insB; ycdA; ycdB; stbB; stbA; ycgA; ycgB; ychA; yciB; ycjA; ycjB; ydaA; ydbA; ydcA; yddA; ysgB; ydaA; ydbA; ydcA; yddA; ssb; ydeA; ydeB; ydgA; yddA; yddB; yeaA; tetR; tetC; tetD; ydeA; yefA; psiB; psiA; mok; hok; yehA; yeiA; 32; X; traM; finp; traU; yfaA; yfiB; yfiC; traC; traE; traB; traB; traD; traU; traX; traZ; trbB; traU; traY; traA; traC; trbB; traU; ygeA; trbC; traX; traZ; trbB; traU; traB; traB; traC; traZ; traB; traC; traX; yieA; finO; yigA; yigB; yihA; repA2; inC; Plasmid R100 (specific_host:Shigella flexneri 2b strain 222, plasmid R100 clasmid R100 specific_host:Shigella flexneri 2b strain 222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26422 ACCCACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ATGGCCGACTTGGCGCGCATGGAAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168;
                    2 (bases 1 to 94281)
Sampei, G. and Mizobuchi, K.
                                                                                   Sampei, G. and Mizobuchi, K. Organization and diversification of plasmid genomes: complete nucleotide sequence of the R100 genome
Direct Submission
                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ACACACTGCGAGGAGGCCAGCCTGGCCGAACACACAGGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid R100 DNA, complete sequence. AP000342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCCTGCCATGCA 26541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(26615.
/note="imperfect"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVBELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQQLIDWHEADKVAGPL
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7506 c 7633 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="beta-lactamase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 164.4; DB 1; Length 26652; Pred. No. 2.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94281 bp
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FEATURES
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                                                           /translation="mSQQANDNSESRFMGLMTRIADKTGALGSVVSAMGCAACFPALA
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/transl_table=11
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/TVLEPYRPLEIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
                                                                                                                                                                                                                                                                                                      /gene="merC"
                                                                                                                                                                                                                                                                                                                            /gene="merC"
1234. .1695
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="100% identical to gp:NRIMER_5[MerP of plasmid NRI]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mennlentrigyfakaagynvetrfygrkgllrepdkpygsir
RYGEADVVRVKFVKSAQRLGFSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="merp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="regulatory protein of mer operon"
/protein_id="BAA78785.1"
/db_xref="GI:5103149"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="merT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARMETVLSELVCACHARKGNVSCPLIASLQGEAGLARSAMP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="100% identical to gp:NRIMER_1[MerR of plasmid NR1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="Escherichia coli strain K-12"
/note="Plasmid R100 is also referred to join(59. .7369,11456. .19730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="terminal IR of Tn21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /specific_host="Shigella flexneri 2b strain
/db_xref="taxon:28399"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /plasmid=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="merT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transposon="Tn21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to as NR1 or R222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid NR1]"
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note="100% identical to gp:R1004\_6[MerA of plasmid R100]"

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repeat_unit
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SGVVALELAQAFARLGAKVTILARSTLFFREDPAIGEAVTAAFRMEGIEVREHTQASQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAGELIQTAALAIRNRMTVQELADQLFPYLTMVEGLKLAAQTFNKDVKQLSCCAG
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/transl_table=11
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/gene="merD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAFLGEHWGVAALALTGLFVLAVTRLLRAFRGGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="100% identical to gp:ECOMERTET_3[urf1, ORF, gene product of plasmid R100]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="yadA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDFGTGYSCLQHLKCCPITTLKIDQSFVARLFDDARDQTIVRAVIQLAHGLGMDVIFR
RRLHQLIGRNGCCAASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAA78792.1"
/db_xref="GI:5103156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="99% identical to
gene product of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(4692. .7369,11456. .15691)
/transposon="In2"
QKRFLTKQKRSLAAFHREVTQVCKAQKLRVPARNTVALRIASLDPRKVIRRREGQDAA
                            /translation="MATDTPRIPEQGVATLPDEAWERARRRAEIISPLAQSETVGHEA
ADMAAQALGLSRRQVYVLIRRARQGSGLVTDLVPGQSGGGKGKGRLPEPVERVIHELL
                                                                                   /product="transposase of In21"
/protein_id="BAA78793.1"
/db_xref="GI:5103157"
                                                                                                                                                                            transl_table=11
                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                      note="100% identical to gp:TTU42226_8 [TniA of Tn21]"
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="yaeA"
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R100]"
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                                                                REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                 Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebalhia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Parry, G., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Parry, G., Quail, M., Rutherford, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Typhi (T18) enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serovar Enterica serov
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18
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   Direct Submission
                                      Parkhill, J.
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                                                                                                          11677608
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                                                                    (bases 1 to 218160)
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NKAALTLRELERWLTLAVGTYHGSVHNGLLOPPAARWAEAVARYGVPAYVTRATSFLV
DFLPILRRTLTRTGFVIDHIHYYADALKPWIARRERWPSFLIRRDPRDISRIWVLEPE
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/insertion_seq="IS1326"
7370. .7395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"NTP-binding protein"
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MPSEPSVIRTYVALLAAMAGAPLRPRPBLPEMEOLALALLRKVGYRMLVIDELHNVLAG
MPSEPSVIRTYVALLAAMAGAPLRPLYGYGTRDAYIAIRSDDQLEMREEPMALPVWEANDD
NSVNRREEINLLREIGNELRIPLYGYGTRDAYIAIRSDDQLEMREEPMALPVWEANDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"100% identical to gp:TTU42226_7 [TniBdeltal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tniBdeltal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHRTLSMAC"
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96.6%;
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Pred. No. 2.5e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/S_typhi/).
Location/qualifiers
                                /note="HCM1.04c"
complement(1876. .2346)
/gene="insB"
                                                                                                               /note="13 bp inverted repeat flanking IS1"
complement(1876. .2346)
  /note="HCM1.04c, insB, possible IS1 transposase,
                                                                                                                                                                                                            complement(1871. .2585)
                                                                                                                                                                                                                                                                                       GIHRAVNGYPLIQSAANQLAVIKRLLGDTKYLDACITENLCMFSPEGYLYLFMQRRFI
                                                                                                                                                                                                                                                         complement(1697.
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/protein_id="CAD09621.1"
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/gene="HCMI.03c"
/note="HCMI.03c, hypothetical protein, len: 107 aa;
unknown function"
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/gene="HCM1.03c"
                                                                                                                                                                                                                                 'note="possible RBS"
                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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/db_xref="GI:16505742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="HCM1.02c, hypothetical protein, len: 103 aa;
unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(742, .1053)
/gene="HCM1.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HCM1.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="possible RBS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MMYPDITGVKMKLSQLEVGMTVWSLSRTKMGNTTIKTVTLHSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRLTYTRLDEELEKIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative membrane protein"
/protein_id="CAD09619.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane-spanning regions. Spans sequence end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HCM1.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="CT18"
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/product="putative magnesium and cobalt transport protein"
/protein_id="CAD09624 1"
/protein_id="CAD09624 1"
/db_xref=="GC:16505746"
/translation="MLSAFQLENNRLTRLEVEESQPLVNAVWIDLVEPDDDERLRLQS
ELGQSLATRPELEDIEASARFFEDDOGLHIHSFFFFEDAEDHAGNSTVAFTIRDGRLF
TLRERELPAFRLYRMARSOSMVDGNAYELLDLFETKIRQLADEIENTSDLEQLSR
VIMEGHOGDEYDEALSTLAELEDIGWKVRLCLMDTQRALNFLYRKARLPGGOLEOARE
LIRDIESLLPHNESSLFQKVRFLMQAAMGFINIEQNRIKIFSVVSVVFLPFTLVASSY
                                                                                                               /note="Pfam match to entry PF01544 CorA, CorA-like Mg2+transporter protein, score 432.90, E-value 2.8e-126" complement (3653. 3656)
                                                                                                                                                                                                                                                                  complement(2697. .3584)
                                                                                                                                                                                                                                                                                                  GMNFEFMPELKWRFGYPAAIIFMILAGLAPYLYFKRKNWL"
/note="possible RBS"
4014. .4343
                                                                                             /note="possible RBS"
                                                                                                                                                                                                                                     /gene="corA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"HCM1.07c, corA, probable magnesium and cobalt transport protein, len: 316 aa; similar to many e.g. SW:CORA_ECOLI (EMBL:L11042), corA, Escherichia coli magnesium and cobalt transport protein (316 aa), fasta scores; E(): 0, 99.1% identity in 316 aa overlap. Contains Pfam match to entry PF01544 CorA, CorA-like Mg2+transporter protein. Contains hydrophobic, possible
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/gene="corh"
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/note="13 bp inverted r
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/gene="insa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="possible translational frameshift site, that determined experimentally (EMBL:X52534)"
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/protein_id="CAD09623.1"
/db_xref="GI:16505745"
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QRWLFYAYDRLRKTVVAHVFGERTMATLGRLMSLLSPFBVVIWMTDGWPLYESRLKGK
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/protein_id="CAD09622.1"
/db_xref="GI:16505744"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAAGAAG 63
                                                                                                                                                                                                                          Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A. Sequence Conservation between Regulatory Mercury Resistance Genes from Mercury Polluted and Pristine Environments
                                                                                                                                                                                                                                                                                                                                         Alcaligenes faecalis.
Alcaligenes faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                      A.faecalis (SE20MERR) merR gene for regulatory protein
                                                                                         Submitted (13-MAY-1994) Osborn A. M.,
Genetics and Microbiology, Liverpool,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                merk; regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                  Z33484.1 GI:607038
                                                                                                                                                    Direct Submission
                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                         Alcaligenes.
                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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4014. .4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein".
/protein_id="0AD09626.1"
/db_xref="G1:16505748"
/translation="MGHYDYTRTLRVQLYDASRFHDGATAEQAGELHTVAFSKPAIAD
DIQKIVDTTAEVLGKRYSVNVFSN"
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/gene="HCM1.10c"
/note="HCM1.10c, hypothetical protein, len: 68 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4363. .4569)
/gene="HCM1.10c"
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/db_xref-"G1.16505747"
/tanslation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
/translation="MAHQLLIGKGMITLNLLRDINSQGQVQMAMNGGILNLTVFDIK
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/gene="HCM1.08"
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                 /organism="Alcaligenes faecalis"
/isolate="SE20"
/db_xref="taxon:511"
/clone="pSE20R1, pSE20R2"
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96.6%;
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Pred. No. 2.3e-26;
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                                                                                                                                University of Liverpool,
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                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                             JOURNAL
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            -10_signal
                                         -35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTTGTAACTCGTGTGCGCCTGCCATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 ACCCACTGCGAGGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
                                                                                                                                                                                                                                                                                                                                merR; regulatory protein.
Enterobacter aerogenes.
Enterobacter aerogenes
                                                                                                                                                                                                                                        1 (bases 1 to 516)
Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A.
Sequence Conservation between Regulatory Mercury Resistance Genes from Mercury Polluted and Pristine Environments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 50.7%;
Similarity 96.0%;
                                                                                                                                                                                                                                                                                                                                                                              Z33488.1 GI:607071
                                                                                                                                                                                                                                                                                                                                                                                                           E.aerogenes merR gene for regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           EAMERGE8
                                                                                                                                              Genetics and Microbiology, Liverpool, Merseyside,
                                                                                                                                                               Submitted (13-MAY-1994) Osborn A. M.,
                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                            Osborn, A.M.
                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                       Enterobacter
                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MENNLENLTIGVFAKAAGVNVETIREVQRKGLLPEPDKPYGSIR
RYGEADVVRVKFVKSAQRLGFSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMAD
LARMETYLSELVCACHARKGNVSCPLIASLQGEGGLARSAMP"
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                                                                        /db_xref="taxon:548"
                                                                                                                                 ocation/Qualifiers
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Pred. No. 7.3e-26;
O: Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 516;
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                                                                                                                                                         UK, L69 3BX
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RESULT 15
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                    Submitted (15-SEP-1998) School of Biological Sciences, University of Liverpool, Crown Street, Liverpool, Merseyside L69 7ZD, UK
                                                                                                                                                                                                                                                                                                                2 (bases 1 to 333)
Bruce, K.D., Lilley, A.K. and Bailey, M.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                        mer sequences on plasmids
                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 333)
Bruce, K.D., Lilley, A.K. and Bailey, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF092069 333 bp DNA linear E
Pseudomonas putida group 2 plasmid MerR (merR) gene,
                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF092069.1 GI:5817323
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                                                                                              /db_xref="taxon:303"
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/note="this plasmid is naturally-occuring but was recovered in a Pseudomonas strain which was introduced into the samples"
                                    complement(<1. .>333)
/gene="merR"
                                                                                        complement(<1. .>333)
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a 138 c 169 g 106 t
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/codon_start=1
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72. .506
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                 124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGG 166
                                                                     105 ATGGCCGACCTGGCGCGCATGGAAACCGTGCTGTCTGAACTGGTGTGCGCCTGCCATGCG 46
                                                                                                                                           165 ACCCACTGCGAGGAAGCCAGCAGCCTGGCCGAGCACAAGCTTCAGGACGTGCGCGAAAAG 106
                                                                                                      64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
45 CGGAAGGGGAATGTTTCCTGCCCGCTGATTGAGTCGCTACAGG
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                                                                                                                                                                                                                                                                                                                   109 c
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91.4%;
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Pred. No. 5.2e-21;
0; Mismatches 14;
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Job time : 1800 secs Search completed: June 2, 2003, 06:52:54

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Listing first 45 summaries
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3632.620 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

U S S 4 D O C 8 Q	Result No.
321 321 321 164.4 164.4 129.2 43.6	Score
100.0 100.0 100.0 51.2 51.2 51.2 40.2 13.6	Query
321 354 509 435 7076 7076 568 3012 8908	Length DB
24 24 13 15 21	DB
ABK52207 ABK52212 ABK52213 ABK52206 AAQ20186 AAQ20186 AAQ86906 AAQ86906 AAQ52054 AAZ52054 AAZ52054	ID
DNA encoding synth DNA encoding pASK-Adjacent plasmid r DNA encoding Shige HlyA gene with ctx Vibrio cholerae di Mercury resistant Codon optimised Hu Packaging construc	Description

40 42 43 44 45	111 111 113 114 115 116 117 118 117 118 118 118 118 118 118 118	10
	41.2 41.2 41.2 41.2 34.4 35.8 36.2 36.2 36.2 36.2 36.2 36.2 36.2 36.2	<u>د</u> د
999977	12.8 12.8 12.8 12.8 12.8 12.8 12.8 12.8	D
4403765 4411529 930 2598 2625 3111	9167 9167 9167 9167 9170 9194 9194 9194 9194 9194 9783 9785 9785 9785 9788 4341 9788 4319 9788 4319 9788 12411 9788 1382 2963 1431 10732 11933 11933 2215	1001
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#### ALIGNMENTS

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CC recombinant DNA molecule comprising a sequence encoding a chelon protein CC which binds mercuric ions. The invention is useful for recombinantly CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC immobilised onto a solid support, is useful for concentrate the heavy CC immobilised onto a solid support, is useful for concentrating heavy metal concombinantly expressed in enteric bacteria (which are nontoxigenic and CC adueous medium including biological fluids. The nucleic acid, when CC adueous medium including biological fluids. The nucleic acid, when CC compathogenic), is suitable for use in the in vivo sequestration and CC elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The mucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic acid sequence encodes the synthetic MerR chelon variant protein of the invention. This sequence encodes one of the heavy metal binding proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 321 BP; 72 A; 94 C; 103 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new non-naturally occurring
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                                                                                                                                                                                                                                                           121 GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321;
                                                                                                                                                                                                                                                                                                       61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTGTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGACACACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60
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                                                                                                                                                                                                                                                                                                                               AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
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                                                CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                   AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 321; DB 2
100.0%; Pred. No. 2e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 321;
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1 ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACCAAGCTCAAGGACGTGCGCGAG 1 ATGACACACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG

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Matches Query Match

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Similarity

100.0%; 0;

Score 321; DB 24 Pred. No. 2.1e-77 Mismatches

DB 24;

Length 354; Indels

0

Gaps

Conservative

Sequence 354 BP; 83 A; 103 C; 111 G; 57 T; 0 other;

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RESULT 2
ABK52212
irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; PCR; pASK-MBD; gene; ds.
                                                                                  divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated argueous medium including biological fluids. The nucleic acid, when a queous medium including biological fluids. The nucleic acid, when necessary is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic cation can be a supposed to the contamination with high affinity. The present nucleic cation such as mercury or cadmium with high affinity.
                                                                                                                                                                                                                                                                                                                                                                                     cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding the chelon protein is useful for binding the chelon protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 24; 42pp; English.
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                                                                   sequence represents the pASK-MBD gene, as described in the
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RESULT 3
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recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                        Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                         The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                            Disclosure; Page 25; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summers AO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy metal binding protein; MerR; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adjacent plasmid region encoding variant MerR protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                 irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; MerR; gene; ds.
                                                                                                                                                                                                                                                             Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                      Shigella flexneri.
                                                                                                                                                                                                                                                                                                    DNA encoding Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                                                     13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                              ABK52206;
                                                                                                                                                                                                                                                                                                                                                                                                                              ABK52206 standard; DNA; 435 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 509 BP; 139 A; 128 C; 140 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 AAGGGGAATGTTTCCTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GCCGACTTGGCGCGCATGGAAACCGTGCTGTGTAACTCGTGTGCGCCTGCCATGCACGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CACTECGAGGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 ATGACACACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                          Location/Qualifiers
                                       /product= "Shigella flexneri wild-type MerR protein"
                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 321; DB 24; Length 509;
Pred. No. 2.2e-77;
); Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
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WO200230962-A2

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ce recombinant DAR molecule comprising a sequence encoding a chelon protein for which binds mercuric ions. The invention is useful for recombinantly certification in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing the nucleic acid encoding the chelon protein is useful for binding certifications, to take up, sequester and concentrate the heavy divalent mercuric ions, to take up, sequester and concentrate the heavy irrigation water of waste streams. The DNA of the invention when certificated environment waster, hydroponic solutions or irrigation water of waste streams. The DNA of the invention when cerombinantly expressed in enteric bacteria (which are nontexispenic and concentration perspenic accombinantly expressed in enteric bacteria (which are nontexispenic and concentration of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The certification such as mercury or cadmium with high affinity. The present nucleic caid of the invention are also useful in water treatment resins. The nucleic acid of the invention with high affinity. The present nucleic certification of heavy metal binding proteins termed chelons.
                                                                              AAQ20186
ID AAQ2
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 EX FX EX
                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001; 2001WO-US31819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                       Sequence 435 BP; 95 A; 113 C; 146 G; 81 T; 0 other;
HlyA gene with ctxB and mer gene inserted
                           31-MAR-1992 (first entry)
                                                      AAQ20186
                                                                                AAQ20186 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-435437/46.
                                                                                                                                                                                                                                                                238
                                                                                                                                                                             124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                         168;
                                                                                                                                                                                                                                   64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                    ACCCACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                               ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACAACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                    51.2%;
96.6%;
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                      Score 164.4; DB 24; Length 435; Pred. No. 3.8e-35; 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                      297
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cholera; vaccine; enterotoxin; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of the haemolysin (hlyA) gene with two genes inserted into it, the cholera toxin subunit B gene (ctxB) and a mercury resistance gene (mer). It is used in the creation of a wishrio cholerae strain that has have 100% efficacy in protecting humans against subsequent infection with a strain of a similar serotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be used for prodn. of vaccines against cholera. It is unclear whether the mer gene sequence is that of the sense or anti-sense strand as neither appears to have a clear reading frame. See also AAQ20185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-007465/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaper JB, Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment encoding toxin, used as vaccines against cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYMA-) UNIV MARYLAND BALTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7076 BP; 1578 A; 1978 C; 1966 G; 1554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 21; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Vibrio cholerae strains - comprise restriction endonuclease
AAQ86906 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                        5604 ACCCACTGCGAGGAGGCCAGCAGCCCGACCAACGAGGACGTGCGCGAGAAG
                                                                                                                                      124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                         64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                    4 ACACACTGCGAGGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAG 63
                                                                                                                                                                                                             CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGCGAAGCAGGC 5777
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-US03812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0533315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "interrupted hlyA gene"
complement (1193..819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "inserted mer gene"
5882..7076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5873..1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /noté= "inserted ctxB gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "resumption of hlyA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . . 633
                                                                                                                                                                                                                                                                                                                                                                                                                           51.2%; Score 164.4; DB 1 96.6%; Pred. No. 6.4e-35;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 7076;
                                                                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                              0
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AAQ86906;

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RESULT 7
AAQ58554
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                                                                                                                                                                                                                                                                                                                  Matches 168;
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local ;
      Mercury resistant control gene merR(1).
                                                                                      AAQ58554 standard; DNA; 568 BP
                                                                                                                                                                                                                                                                                                                                                                                                                           New avirulent Vibrio cholerae strains of a non-01 serogroup can be used in vaccines to protect against cholera caused by non-01 strains. The new strains are derived from the 0139 serotype and the DNA encoding mercury resistance and the cholera toxin B subunit are necessary resistance and the cholera toxin B subunit are that the new strains are immunogenic, inducing a strong local immunity and the mercury resistance gene allows the vaccine strain to be identified without the use of antibiotics. The new strains do
                                     16-SEP-1994
                                                             AAQ58554;
                                                                                                                                                                                                                                                                                                                                                             Sequence 7076 BP; 1578 A; 1975 C; 1968 G; 1555 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  not revert to the cholera toxin positive phenotype. For treatm approx. 1 million organisms are taken orally, in aqueous NaHCO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Figure 21; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New avirulent strains of Vibrio cholerae expressing toxin B sub:unit - are stable against reversion and useful in oral vaccines to induce local protective immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-161574/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae; avirulent; serogroup; immunogenic; vaccine; cholera; toxin; mercury resistance; cholera toxin B subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae disrupted haemolysin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                              5724 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGCGAAGCAGGC 5777
                                                                                                                                                                                                 124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levine MM;
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0133438.
93US-0133439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US11424,
                                                                                                                                                                                                                                                                                                                         51.2%;

    Mismatches

                                                                                                                                                                                                                                                                                                                          Score 164.4; DB 16; Length 7076; Pred. No. 6.4e-35;
                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                   AAZ52054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 40.2%; Score 129.2; DB 1 Best Local Similarity 78.3%; Pred. No. 1.3e-25;
Codon optimised Human immunodeficiency virus pol coding region.
                                                                             18-JUL-2000
                                                                                                                                           AAZ52054;
                                                                                                                                                                                         AAZ52054 standard; DNA; 3012 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 568 BP; 130 A; 150 C; 164 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The mercury resistance genes can be used as selectable markers when used to transform other bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-077131/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR49668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AKIT-) AKITA KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Resistance; mercury; selectable marker; Thiobacillus ferrooxidans; transformation; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·35_signal
                                                                                                                                                                                                                                                                                                                                                 506 GGTGACCGAGCCACTTGC 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 CGAAAGGGGAACGTTTCCTGCCCGCTAATTGCGTCACTAAAAAATCGCGCAGCGTGTCCG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCAC 183
                                                                                                                                                                                                                                                                                                                                                                                                            184 TGCGAGGAGGCCAGCAGC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 ATGGCCGACTTGGCGCGCATGGAGGCCGTGCTGTCCGAGCTTGTGTGCGCCTGCCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 ACCCACTGCGATGAAGCCAGCCACTTGGCCGAGCACAAGCTCCAGGACGTGCGCGAAAAG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
                                                                    (first entry)
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89..568
/*tag=
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46..51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
76..79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 23..28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
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HIV; gag; packaging cell line; lentivirus; retroviral vector particle;

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2583 GTCCCAGGGCGTGATCGAGTCCATGAACAAGGAGGTGAAGAAGAATCATCGGCCA 2636

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The patent discloses new packaging cell line for producing a viral cacessory protein independent lentivirus, preferably cell accessory protein independent lentivirus, preferably cell accessory protein independent lentivirus, preferably rector particles. The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a lentivirus, preferably HIV, gagpol, cell the coding sequence for a retroviral nucleotide sequence comprising the coding sequence for a heterologous envelope protein and a cell interest and lentivirus, preferably HIV, cis-acting sequence of cell interest and lentivirus, preferably HIV, cis-acting sequence for a heterologous envelope protein and a cell cell interest and lentivirus, preferably HIV, cis-acting sequences required for packaging cell lines and viral particles can be used for gene cell therapy or gene replacement with improved safety. They can also be used in the development and production of vaccines and blochemical reagents. The present sequence is a pol coding region of codon optimised HIV cell line. Codon optimisation results in improved expression of the gagpol protein and reduces the risk of recombination between the transfer cell line codon and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination between the transfer cell protein and reduces the risk of recombination protein and reduces the risk of recombination between the tra
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pol; gene therapy; gene replacement; vaccine; biochemical reagent;
codon optimisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray JT, Mulligan RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-1998;
12-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 43; Fig 9; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New packaging cell line for producing a viral accessory protein independent HIV derived retroviral vector particles, useful in therapy or gene replacement -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY70602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3012 BP; 679 A; 1017 C; 892 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector and gagpol mRNA.
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                                                                                                                                                                                                                                                                2403 CGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCCTGCTGAAGCTGGCCGG 2462
                                                     2523 GAAGGCCGCCTGCTGGTGGGCCGGCATCAAGCAGGAGTTCGGCATCCCCTACAACCCCCA
                                                                                                                                                                                                           72 CTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGG 131
                                                                                                                                                                                                                                                                                                                     12 CGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 71
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 245
                                                                                                       GAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGA 191
                                                                                                                                                            CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCTCCAACTTCACCTCCACCACCGT 2522
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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98US-0100063.
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/product= "pol protein"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                         13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 43.6; DB 21; Length 3012; Pred. No. 0.022;
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RESULT 9
AAZ52055
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AC AAZ5
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                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
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                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                       polyA_site
WPI; 2000-271455/23
                    Gray JT,
                                                                                               10-SEP-1999;
                                                                                                                  23-MAR-2000.
                                                                                                                                        WO200015819-A1
                                                                                                                                                                                                                                    rep_origin
                                                               11-SEP-1998;
12-SEP-1998;
                                         (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gag;
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                packaging cell line; lentivirus; retroviral vector particle; therapy; gene replacement; vaccine; blochemical reagent; construct; plasmid; pHDMHgpm2; cycllo; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         construct pHDMHgpm2 DNA.
                     Mulligan RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus macaque polyoma virus.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                   /product= "
5710..6469
                                                              98US-0100022.
98US-0100063.
                                                                                               99WO-US20675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 97..679
                                                                                                                                                                        /*tag= 1
/ote- "This region consists of the gagpol overlap
and cis-acting signals necessary for translation of
                                                                                                                                                                                                                                    /*tag= j
/product= "beta-lactamase (bla)"
8796..8908
                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= d
761..1303
                                                                                                                                                             pol which are not optimised"
                                                                                                                                                                                                        2583..2819
                                                                                                                                                                                                                                                                                         /label= Human_betaglobin_sequence
5897..5921
                                                                                                                                                                                                                                                                                                                                                       /product= "Codon
2613..5624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= a
label= CMV_enhancer/promoter
                                                                                                                                                                                                                'label SV40_origin_of_replication
                                                                                                                                                                                                                                                                                                                                                                                     318..2820
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label= Human_betaglobin_sequence
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                                                                                                                                                                                                                                                                                                                                                                 optimised gag"
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RESULT 10
ABK91609
ID ABK91609
ID ABKS
XX ABKS
AC ABKS
XX ABKS
XX HIV
DE MODI
XX HIV
KW Env
KW acqu
XX Syni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC accessory protein independent lentivirus, preferably

CC human immunodeficiency virus (HIV), derived retroviral vector particles.

CC The packaging cell line comprises a mammalian cell, a retroviral DNA

CC comprising a coding sequence for a lentivirus, preferably HIV, gagpol,

CC where the coding sequence has been mutagenised to improve expression of

CC the viral gagpol proteins, a second retroviral nucleotide sequence

CC comprising the coding sequence for a heterologous envelope protein and a

CC interest and lentivirus, preferably HIV, cis-acting sequence of

CC interest and lentivirus, preferably HIV, cis-acting sequences required

CC The packaging, reverse transcription and integration.

CC The packaging cell lines and viral particles can be used for gene

CC therapy or gene replacement with improved safety. They can also be used

CC the present DNA is that of a packaging construct pHNMHgpm2 which

CC comprises a codon optimised HIV gagpol. The plasmid is defective for the

CC production of the viral envelope and accessory proteins e.g. tat, vif,

CC vpr, rev and Rev response element (RRE). It also lacks the viral

CC cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                    25-APR-2002
                                                                                                                                                           HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS;
                                                                                                                                         acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL
                                                                                                                                                                                                                            Modified HIV protein-encoding plasmid DNA #161.
                                                                                                                                                                                                                                                                               14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                             ABK91609 standard; DNA; 7897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8908 BP; 2134 A; 2579 C; 2355 G; 1840 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses new packaging cell line for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy or gene replacement -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New packaging cell line for producing a viral accessory protein independent HIV derived retroviral vector particles, useful in gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5195 GTCCCAGGGCGTGATCGAGTCCATGAACAAGGAGCTGAAGAAGATCATCGGCCA 5248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5135 GAAGGCCGCCTGCTGGTGGGCCGGCATCAAGCAGGAGTTCGGCATCCCCTACAACCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 GAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 CTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCCTGCTGAAGCTGGCCGG 5074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCTCCAACTTCACCTCCACCACCGT 5134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                        (first entry)
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49.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                              HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chuman immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABR91449-ABR91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                   Synthetic
                                                                                                                                                                                              14-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                     ABK91616 standard; DNA;
                                                                                                                                                        Modified HIV protein-encoding plasmid DNA #168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7897 BP; 1943 A; 2213 C; 2113 G; 1628 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid molecule encoding a modified HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified human immunodeficiency virus Env, Gag, its encoded protein, useful as vaccines for genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                           4459 GAGCCAGGGCGTGATCGAGAGCATGAACAAGGAGCTGAAGAAGATCATCGGCCAGGTG 4516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4339 CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCAGCAACTTCACCAGCACCACCACCGT 4398
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RESULT 12
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Best Local (
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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                                            HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9166 BP; 2227 A; 2662 C; 2513 G;
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              Synthetic
                                                                                                                       Modified
                                                                                                                                                         14-AUG-2002 (first entry)
                                                                                                                                                                                               ABK91619
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                                                                                                                  HIV protein-encoding plasmid DNA #171.
                                                                                                                                                                                                                                                                                                                                                                                            GAAGGCCGCCTGCTGGTGGGCCGGCATCAAGCAGGAGTTCGGCATCCCCTACAACCCCCA 5747
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14-NOV-2000;
28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag. Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or ABCS1449-ABCS1624 represent modified HIV protein-encoding house the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the subsequent of the s
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; 2001US-279257P.
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                                                                                                                                                                                           (first entry)
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.

Modified HIV

protein-encoding plasmid DNA #169.

Synthetic

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KW XE XXX
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Best Local :
HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS;
                                                          Modified HIV protein-encoding plasmid DNA #166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTI) response against native HIV Env, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or LTDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                                                                        14 - AUG - 2002
                                                                                                                                            ABK91614;
                                                                                                                                                                      ABK91614 standard; DNA; 9170 BP
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14-NOV-2000;
28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 769-772; 794pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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Best Local Similarity
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    14-AUG-2002
                                            ABK91607;
                                                                            ABK91607 standard; DNA; 9189 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
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14-NOV-2000;
28-MAR-2001;
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Modified HIV protein-encoding plasmid DNA #159

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
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#### ALIGNMENTS

ACCESSION VERSION KEYWORDS COMMENT REFERENCE SOURCE DEFINITION AUTHORS TITLE JOURNAL ORGANISM Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL108460
AL108460.1 GI:5628764
GSS. - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP). http://www.edgp.ebi.ac.uk...This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector Drosophila melanogaster.

Drosophila melanogaster

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Neoptera; Drosophilidae; Drosophila. Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Direct Submission Genoscope. (bases 1 to 1101)

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39 39 38.2 40.6

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CNS017SY BE402139 BQ607497 B1341447 BH179075 CNS07L8T

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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTG
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                                                                                                                                                                                                                                                                                           Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier, S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE402139.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE402139 587 bp mRNA linear EST 21-JUL-2000 CSB004H01F990908 ITEC CSB Wheat Endosperm Library Triticum aestivum
                                                                                                                                      Email: rudi@pi.csiro.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                 Tel: 61 62 465496
Fax: 61 62 465000
                                                                                                                                                                                                                                        Div. of Plant Industry, CSIRO Canberra ACT 2601 AUSTRALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Poolideae
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/organism="Drosophila melanogaster"
/ob_xref="taxon:7227"
/clone="BACN37L08"
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/plasmid="pBeloBAC11"
/note-"end : SP6"
176 c 160 g
/cultivar="Wyuna"
/db_xref="taxon:4565"
/clone="C58004H01"
/clone_lib="ITEC CSB Wheat Endosperm Library"
                                                                                                                       Loca1
                                                                             organism-"Triticum aestivum"
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RESULT 3
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BRY_3391 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.
BQ607497
                                                                                                                                                                                                                                The Arabidopsis Information Resource Carnegie Institution of Washington, Dej 260 Panama Street, Stanford, CA 94305, Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
                                                                                                                                                                                                                                                                                                                                           interpreting wheat EST sequences Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                  Clarke, B., Lambrecht, M. and Rhee, S. Assessing the utility of Arabidopsis genomic information for
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bread wheat.
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a 218 c 185 g 71 t
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/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
                 /organism="Triticum aestivum"/cultivar="Wyuna"
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                     /clone_lib="wheat EST endosperm library"
                                                                                                                            /db_xref="taxon:4565"
                                                                                        /tissue_type="endosperm"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing. Bases called and alt_trimmed with phred v0.989904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPi
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 CAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI341447 524 bp mRNA linear 368872 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 180 c 165 g 95 t
                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                       /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                            1. .524
                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
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                                          11.9%;
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                        0;
                                        Score 38.2; D
Pred. No. 5.5;
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554 AGGCCAACGATGGCTGGGTGGCATGGTGCAGCACTATTTCGCCAGCGCCTGGCTGCGCM 613
                                        239 TGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCAC 298
                                                                                494 CCAAGTTCCAGAAGGTCGAGTTCAGCGCCCTGGACAAGGACAAGGCCGAGTTCGAGAAGC 553
                                                                                                                        179 CCCACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 GCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAAGGACGTGCGCGAAGAAGATGGCCG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 736.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-
Tel: (33) (0)3 2087788
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Le Paslier,M.-C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library denomics 65 (2), 87-94 (2000)
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 013 row: D column: 05
Seq primer: M13 reverse primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS sequencing ID=DGOAA013CB03BP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Pierce RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: 013_D_05-21
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[ bases 1 to 736)
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736 bp DNA linear GSS 19-00
013_D_05-rev SmBAC1 Schistosoma mansoni genomic clone 013D05
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                                                                                                                                                                             Conservative
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253 c 247 g 99 t 5 others
                                                                                                                                                                                                                                                                                                                              /dev_stage="cercariae"
/lab_host="Blomphalaria glabrata"
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="SmBAC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:6183"
/clone="013D05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Puerto-Rican"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schistosoma mansoni"
                                                                                                                                                                                               55.5%;
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    Mismatches

                                                                                                                                                                                               Score 38; I
Pred. No. 7;
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                                                                                                                                                                                                                                                              299 GAAAGGGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

- Web : www.genoscope.cns.fr)
Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC II vector and used to transform E. coll DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
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                                                                                BE636656 716 bp mRNA linear EST 03-JAN-2002 rockefeller 0.321 Mastigamoeba balamuthi lambda ZAP II Library
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BE636656
BE636656.1 GI:9919767
                                           mRNA sequence.
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                                                             Mastigamoeba balamuthi cDNA similar to small heat shock protein,
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/note="end : T3"
253 c 247 g
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/db_xref="taxon:6183"
/clone="013CB03"
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55.5%;

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mastigamoeba balamuthi. Mastigamoeba balamuthi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba
1 (bases 1 to 716)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmuller@rockvax.rockefeller.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Rockefeller Universit
                                     i (bases 1 to 710)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
pevelopment of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                          HVSMEh0100J10f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0100J10f.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Biochemical Parasitology
                 Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:9859525.
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                     Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCGIGCIGICIGAACICGIGIGCGCCIGCCAIGCACGAAAGGGGGAAIGITICCIGCCCG 147
                                                                                                                                                                                       Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCCAGCAGCCTGGCC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 260
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/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
228 c 214 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mastigamoeba balamuthi"
/strain="ATCC 30984"
Wing RA
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Pred. No. 7
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KEYWORDS
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                                                                                                                                                            BF484898
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                       221 AGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 ACCGCGTCGGCGA 168
                                                                                                                                                                                                                                                                                               281 TGTGCGCCTGCCA 293
                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                        WHE2320_H06_P12ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2320_H06_P12, mRNA sequence.
                                         BF484898.1 GI:11568199
                                                                                                                                    BF484898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Total hq bases = 229
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                                                                                                                                                                                                                                                                                                                              AGGACGAGGTGGCGAGCATGGACCGGCGCCCCGCTCCTCGACCTCGGGCCACCCGCTCCTCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //OCTE—"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; //OCTE—"Vector: lambdaZAP; Site_1)  
Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson Prisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of bired value 20 or above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) 209 c 238 g 106 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                above. For more details on library preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP)"
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/lab_host="SOLR"
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/clone="HVSMEh0100J10f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hordeum vulgare"
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Pred. No.
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BQ805185.1 GI:22029394
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        339 AGCCCCTCGGCCCCGGCGAGGACACCTACATCTACAGGGGCGAG 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 ACGCCTTCGCCGGGCTGATGATCACGGCGGCGTTCCTGTCGGCCTGCGGCTTCTGCGCCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCG 70
WHE3563_G11_M21ZS Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3563_G11_M21, mRNA sequence.

BQ805185
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes Pre-anthesis spike cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone_lib="Wheat pre-anthesis spike cDNA library"/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i (bases 1 to 538)
Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossnan, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                     11 GCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCG 70
                                                                                                                                                                                                                                          107;
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//note="Wector: Lambda ZAP II, excised phagemid; Site_1:
//note="Wector: Lambda ZAP II, excised phagemid; Site_1:
//note="Wector: Lambda ZAP II, excised phagemid; Site_1:
//note="Wector: Lambda ZAP II, excised phagemid; Site_1:
//note="Wector: Lambda ZAP II, excised phagemid; Site_1:
//note="Wector: Lambda ZAP II, excised phagemid; Well-watered, with post-anthesis
//note="Wector: Environment 2" 240C/170C day/night, well-watered, with post-anthesis
//note="Siterilizer" Environment 4" 370C/170C
//note="Siterilizer" Environment 4" 370C/170C
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/cultivar="Butte 86"
                                                                                                                                                                                                                                                                                                                                                                                                                                    preparations and DNA sequencing were performed Anderson lab (others)."
180 c 197 g 66 t
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/tissue_type="whole grains"
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                          188 AGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACT 247
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                                                                                                                                                                                                                                                                                                                                                                                                 128 AGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCG 187
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with those of corresponding noncancerous liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with the liver with
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1 (bases 1 to 640)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Zeguang Han
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/clone_lib="GLC"
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/dev_stage="Adult"
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Pred. No. 14;
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                              253 CGCATGGAAACCGTGCTGTCTGA 275
                                                                                                                                   134 CAGCTGCGCGACGCGGTGCGCAAGTGGGTGGACAAAGCCTATGACTTCGAGCGCCGGCGC 193
                                                                            194
                                                                                                                                                                    133 AATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAG 192
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                                                                                                                                                                                                                                          73 TTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 22 High quality sequence stop: 304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-HT0059-
270899-010-H08&t3=1999-08-27&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 304) HCGP http://www.ludwig.org.br/ORESTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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CTCATGGGCCTGGCCGTGCCAGA 276
                                                             GCCATCGTCAAGGCGGGCGGCTACTCCAAGGAGGCCTGGGGCGAGATGGCTGAGCTGGGT 253
                                                                                               GCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCG 252
                                                                                                                                                                                                        TCGGCGCTCAGATGACCCTGGGGGTGTGAGATGGACTTCGACTTCACCGACGAACAGGAA 133
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                              /note="organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
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47.6%;
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181 CGCGGGTGCAGGCGGGGGAGCGCTGGCCCAGTGCTGCGGCATGCCG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 CAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAACCG 265
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Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                    BG857743 707 bp mRNA lir
1024053G04.xl C. reinhardtii CC-1690, normaliz
Chlamydomonas reinhardtii cDNA, mRNA sequence.
BG857743
                                                                                                 EST.
Chlamydomonas reinhardtii.
                                                                                                                                                          BG857743.1 GI:14238927
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Contact: Erika Asamizu
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127 c 113 g 45 t
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Best Local 9
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                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 AGCCTGGACGAGAACGTGCTCATGCAGCTGCGCGAGGCGCCAGTCCGACAACATGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 GAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 AACGAGCAGATGTACAGCCTGCTGGCGGTGTGCCTGGCGCTGTGCCCCGCGGCCGAAG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AATGTTT 313
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 707)
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Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Charles Hauser
                                                                                                                                                                                              BM488564 167 OFFEB-2 pgm2n. pk008. bl1 Normalized Chicken Breast Muscle, Leg Muscle, an Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus CDNA clone pgm2n. pk008.bl1 5' similar to gb|AAH09268.1|AAH09268 (BC009268) Similar to RIKEN CDNA B230113C15 gene [Homo sapiens],
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                   EST
                                                                                                                          BM488564
BM488564.1 GI:18609495
                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGGCGCGCATGGAAACCGIGCTGTCTGAACTCGIGTGCGCCTGCCATGCACGAAAGGGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
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919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chauser@duke.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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49.78;
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COMMENT
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Search completed: June 2, 2003, 06:22:43 Job time: 1520 secs
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.3%;
Best Local Similarity 47.2%;
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                                                                                                                                                                             178 CAGTTGGCCCAGCAGTGGATCGACCGCATCCAGAGCTGCTTATCGGACGCCTGAGAGCCT
                                                                                                                                                                                                                                                                  118 AAAGCGTTCTTCGATCTGAAGACGACGAAACGCGTTTACAACTTCTGCGCCCAGGACGTG
                                                                                                                                  193 GCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCC 243
                                                                                                                                                                                                                        133 AATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                    109;
                                                                                                                                                                                                                                                                                                           73 TTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGG 132
                                                                                                                                                                                                                                                                                                                                                          58 GAGGTGGAGTCCATCACGCCCGGAACCCCCACCATGGGGGCCCCGGAAGACGGTGGACGAG 117
                                                                                                                                                                                                                                                                                                                                                                                                     13 GAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cogburn, L.A. and Monsonego-Ornan, E. ESTs from Normalized Chicken Breast Muscle, Leg Muscle, Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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Townsend Hall, Newark, DE 19717, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Larry A.
                                                                                       CTCAGGGAGAGCCCCCAACCCACGCACGGTCNTCTGCAGCGGAACAGAGCC 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; uvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

142 c 158 g 65 t 13 others
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growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Epiphyseal Growth Plate cDNA library (pgm2n)/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Commercial broiler and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="pgm2n.pk008.b11"
/clone=1ib="Normalized Chicken Breast Muscle, Leg Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Pred. No. 10
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QΥ
                                                                                                                                  The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC the 5'-end sequence/3'-end sequence is selected from those defined in CC in gene therapy. The primers sets can be used in antisense therapy and CC particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, CC detection and/or diagnosis of the abnormality of the proteins encoded by CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB1563 to AAH13674 represent human cDNA sequences; and AAH13628 and CC AAB1563 and AAH1363 to AAH13628 and AAH1363 to AAH13628, all of which are used in the exemplification of the present human cnown sequences; and AAH13629 to AAH13632 of the present invention.
                                          Matches
                                                          Query Match
Best Local
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AAH14532/c
                                                                                                   Sequence 4147 BP; 1078 A; 1016 C; 1118 G; 935 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 12080; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH14532;
179 CCCACTGCGAGGAGGCCA 196
                             tch 5.6%; Score 18; DB al Similarity 100.0%; Pred. No. 13; 18; Conservative 0; Mismatches
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, Sugiyama T, Wakamatsu A, Nagai F
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                                                                DB 22; Length 4147;
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K, Otsuki T;
                                 0; Indels
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Db 1159 CCCACTGCGAGGAGGCCA 1142

Search completed: June 2, 2003, 08:39:1: Job time: 203 secs

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RESULT 13
ABQ90147/c
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Cc specification, but was obtained in electronic format directly from WIPO at format of information in formations.
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. capsulatus gene #132 for DNA array.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ90147 standard; DNA; 2595 BP
                                                                                                                                       Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200255655-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylococcus capsulatus
The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of
                                                                                                                                                                                                                                WPI; 2002-557818/59.
                                                                                                                                                                                                                                                                  Salzberg SL;
                                                                                                                                                                                                                                                                                          Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-2001; 2001NO-0000235.
12-JAN-2001; 2001NO-0000239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2002; 2002WO-NO00019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002.
                                                                               Claim 19; Page 115-116; 678pp; English.
                                                                                                                      capsulatus genes
                                                                                                                                                                                                                                                                                                                                                        (TIGR-) TIGR.
                                                                                                                                                                                                                                                                                                                                                                              (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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100.0%; Pred. No.
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Fraser CM, Du
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                                                                                                                                                                                                                                                                                                                      Lien
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2956 CTGGCCGAACACAAGCTC 2973

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                                   Matches
                                                Best Local
                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2595 BP; 442 A; 737 C; 885 G; 531 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL23967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL23967 standard; DNA; 3873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 23374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The inventuation in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 23374; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001.
                                                                                             Sequence 3873 BP; 998 A; 1083 C; 996 G; 796 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting genes from Drosophila and for elucidating cell signalling
                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                      interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
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 28 CTGGCCGAACACAAGCTC 45
                                   18;
                                                   Similarity
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                                   Conservative
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                                                  5.6%; Score 18; DB 23; Length 3873; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
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                                      Mismatches
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and cell-cell
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05-DEC-
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08-DEC-
08-DEC-
             WPI; 2001-483426/52.
                                 (HUMA-) HUMAN GENOME SCI INC
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20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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                       Barash SC,
                                           2001US-0259678.
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2000US-0246527.
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2000US-0246474.
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2000US-0241785.
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                                                                                                                                                                                                                                                                                                                       2000US-0241786.
                                                                                                                                                                                                                                                                                                                   2000US-0241787
                                                                                                                                                                                                                                                                                                                                       2000US-0240960.
                      Ruben SM;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

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RESULT 12
AAS82310/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic c activity, and can be used in gene therapy and vaccine production. (I) createns and polynucleotides may be used in the prevention, diagnosis and c treatment of diseases associated with inappropriate (I) expression. For c example, they may be used to treat disorders associated with decreased c that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) c polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the c protein. (I) proteins and polynucleotides may be used to prevent, c diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic diseases, especially c to AAK87694 represent human immune/haematopoietic antigen genomic c sequences from the present invention. AAK34942 to AAK34950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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Best Local (
polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                      Claim 1; SEQ ID No 18114; 103pp; English.
                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                  The invention relates to isolated polynucleotide (I) and
                                                                                               biodiversity
                                                                                                                                                                                     P-PSDB; ABG18123.
                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #18114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS82310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS82310 standard; cDNA; 1536 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1231 BP; 293 A; 259 C; 316 G; 363 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 42287; 3071pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840 GAGGCCAGCAGCCTGGCC 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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. 13;
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RESULT 11
AAK8775
ID AAK8775
AC AAK87
AC AAK87
XX Human
XX Human
XX Human
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XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                  cc which binds mercuric ions. The invention is useful for recombinantly cc which binds mercuric ions. The invention is useful for recombinantly cc cell capable of expressing a chelon coding sequence with a vector cc comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding cc make the protein to produce a recombinant host cell and culturing cc metal ions from contaminated soil, ground water and concentrate the heavy cc irrigation water of waste streams. The DNA of the invention, when cc immobilised onto a solid support, is useful for concentrating heavy metal considered environment waste streams or contaminated concentrated available for use in the invention and cc nonpathogenic), is suitable for use in the in vivo sequestration and cc endimination of mercuric ion from gastrointestinal tracts of animals or cellmination of the invention are also useful in water treatment resins. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent caid sequence represents synthetic product 1 forward PCR primer that was used in the methods of the invention for construction of pask-MBD vector.
                                                                                                                                                                                                                                                                                           밁
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-435437/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000; 2000US-240465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33 BP; 8 A; 8 C; 12 G; 5 T; 0 other;
                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42287.
                                                                                                                                                                          07-NOV-2001 (first entry)
                                                                                                                                                                                                                           AAK87475 standard; DNA; 1231 BP
                                                   WO200157182-A2.
                          09-AUG-2001.
                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                    1 ATGACACACTGCGAGGAGG 19
                                                                                                                                                                                                                                                                                           ATGACACACTGCGAGGAGG
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                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 19; DB 24; Length 33; 100.0%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                  Mismatches
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         01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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22-AUG-2000;
23-AUG-2000;
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08-SEP-2000;
12-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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28-JUN-2000;
        14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
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29-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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14-AUG-2000;
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01-SEP-2000;
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22-AUG-2000;
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14-AUG-2000;
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14-SEP-2000;
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2000US-0180628.
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2000US-0216647.
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                          2000US-0236369
                                     2000US-0236368
                                                                2000US-0236327
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17-JAN-2001; 2001WO-US01354.

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RESULT 9
AAQ58554
ID AAQ5
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AC AAQ5
XX
DT 16-S
XX
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Best Local
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                    16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                         humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic acid sequence represents synthetic product 2 forward PCR primer that was used in the methods of the invention for construction of pASK-MBD vector.
                                                                                                  AAQ58554 standard; DNA; 568 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 30 BP; 7 A; 11 C; 8 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 24; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; pASK-MBD; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001; 2001WO-US31819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200230962-A2
                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                              160 CTACAGGGATCCTCAGGCACCCACTGCGAG 189
                                                                                                                                                                                                         1 CTACAGGGATCCTCAGGCACCCACTGCGAG 30
                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                ilarity 100.0%;
Conservative
                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caguiat JJ;
                                                                                                                                                                                                                                                                                                                9.3%; Score 30;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                     DB 24;
                                                                                                                                                                                                                                                                                                                  7.8e-06
                                                                                                                                                                                                                                                                                                                                  Length 30;
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                    Gaps
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В
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                 Query Match
                                                              irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                 WO200230962-A2
                                        Synthetic
                                                             heavy metal
                                                                                                Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                     Synthetic product 1 forward PCR primer for construction of pASK-MBD
                                                                                                                                                                                         ABK52208 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                 Sequence 568 BP; 130 A; 150 C; 164 G; 124 T; 0 other;
                                                                                                                                               13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                      The mercury resistance genes can be used as selectable markers when used to transform other bacteria.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 2; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                             Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR49668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-077131/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP06000083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Resistance; mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mercury resistant control gene merR(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35_signal
                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                             383 AAGATGGCCGACTTGGCGCGCATGGA 408
                                                                                                                                                                                                                                                         61 AAGATGGCCGACTTGGCGCGCATGGA 86
                                                                                                                                                                                                                                                                                            26;
                                                        binding protein; pASK-MBD; PCR; primer; ss.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
89..568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
76..79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
46..51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= merR(1) gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
                                                                                                                                                                                                                                                                                                   8.1%; Score 26; DB 15; 100.0%; Pred. No. 0.0009;
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                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                   0.0009;
                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                            Length 568;
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                      Gaps
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18-APR-2002

31-MAR-1996

(first entry)

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XEXTXEX
                                                                                                                   ABK52209/c
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae disrupted haemolysin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9510300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholera; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7076 BP; 1578 A; 1975 C; 1968 G; 1555 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunity and the mercury resistance gene allows the vaccine strain to be identified without the use of antibiotics. The new strains of not revert to the cholera toxin positive phenotype. For treatment, approx. 1 million organisms are taken orally, in aqueous NaHCO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding mercury resistance and the cholera toxin B subunit are inserted into a haemolysin gene. Expression of the B subunit ensures that the new strains are immunogenic, inducing a strong local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used in vaccines to protect against cholera caused by non-01 strains, optionally together with CVD111 which protects against 01 strains. The new strains are derived from the 0139 serotype and the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Figure 21; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New avirulent strains of Vibrio cholerae expressing toxin B sub:unit - are stable against reversion and useful in oral vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-161574/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaper JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New avirulent Vibrio cholerae strains of a non-01 serogroup can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             induce local protective immunity
           Synthetic product 1 reverse PCR primer for construction of pASK-MBD
                                            13-AUG-2002 (first entry)
                                                                        ABK52209;
                                                                                                     ABK52209 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                          5667
                                                                                                                                                                                                                                                                                                   5607 CACTGCGAGGAGGCCAGCCTGGCCGAACACACACGTCAAGGACGTGCGCGAGAAAGATG 5666
                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                               161;
                                                                                                                                                                                                                                                                                                                               7 CACTGCGAGGAGGCCAGCCTGGCCGAACACACCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                                                                                                                                        GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                        AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                                                                                        GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 5726
                                                                                                                                                                              Levine MM;
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0133438.
93US-0133439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US11424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; avirulent; serogroup; immunogenic; vaccine; mercury resistance; cholera toxin B subunit; ss.
                                                                                                                                                                                                                                                                                                                                                          100.0%; +1
                                                                                                                                                                                                                                                                                                                                                                             50.2%; Score 161; DB 16; Length 7076; 100.0%; Pred. No. 3e-74;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For treatment,
                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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EXTXEX

13-AUG-2002 (first entry)

Synthetic product 2 forward PCR primer for construction of pASK-MBD

Ħ ABK52210 RESULT 8

ABK52210 standard; DNA; 30 BP

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CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC immobilised onto a solid support, is useful for concentrating heavy metal CC ions from contaminated environment waste streams or contaminated CC caqueous medium including biological fluids. The nucleic acid, when CC recombinantly expressed in enteric bacteria (which are nontoxigenic and CC compathogenic), is suitable for use in the in vivo sequestration and CC elimination of mercuric ion from gastrointestinal tracts of animals or CC elimination of mercuric ion from such as mercury and/or cadmium. The CC molecules of the invention are also useful in water treatment resins.

CC molecules of the invention are also useful in water treatment resins.

CC cation such as mercury or cadmium with high affinity. The present nucleic cation such as mercury or cadmium with high affinity. The present nucleic acid sequence represents synthetic product 1 reverse PCR primer that was CC used in the methods of the invention for construction of pASK-MBD vector.
                               Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; pASK-MBD; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy divalent mercuric ions, to take up, sequester and concentrate the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001; 2001WO-US31819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                   Sequence 33 BP; 7 A; 9 C; 11 G; 6 T; 0 other;
                                                                        Local Similarity
                                    33;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caguiat JJ;
100.0%; Preu....
+1ve 0; Mismatches
                                                                                                                      10.3%;
                                                                                                                           Score 33; DB 24;
                                                                                           2.1e-07;
                                                                                                                               Length 33;
                                                  Indels
                                                  0;
                                                      Gaps
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RESULT 5
AAQ20186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing CC region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed. CC divalent mercuric ions, to take up, sequester and concentrate the heavy contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when consisted environment waste streams or conteminated contaminated environment waste streams or contaminated consistent including biological fluids. The nucleic acid, when creaming the pressed in enteric bacteria (which are nontoxigenic and CC enumantion of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. CC molecules of the invention are also useful in water treatment resins. CC cation such as mercury or cadmium with high affinity. The present nucleic acid sequence encodes the Shigella flexneri wild-type Merk protein of the convention. This sequence was used in the methods of the invention for the production of heavy metal binding proteins termed chelons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 161; Conservative
          HlyA gene with ctxB and mer gene inserted
                                                                 31-MAR-1992
                                                                                                                AAQ20186;
                                                                                                                                                      AAQ20186 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 435 BP; 95 A; 113 C; 146 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                                                                                                                                                                                                                                                             127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 300
                                                                                                                                                                                                                                                                                                                                                                                                      67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                    AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 401
                                                                                                                                                                                                                                                                                                                                                         GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.2%; Score 161; DB 24; Length 435; 100.0%; Pred. No. 3.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                 AAQ86906
                                                                                            RESULT 6
                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
AAQ86906;
                                        AAQ86906 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7076 BP; 1578 A; 1978 C; 1966 G; 1554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of the haemolysin (hlyA) gene with two genes inserted into it, the cholera toxin subunit B gene (ctxB) and a mercury resistance gene (mer). It is used in the creation of a Vibrio cholerae strain that has have 100% efficacy in protecting humans against subsequent infection with a strain of a similar serotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be used for prodn. of vaccines against cholera. It is unclear whether the mer gene sequence is that of the sense or anti-sense strand as neither appears to have a clear reading frame. See also AAQ20185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 21; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Vibrio cholerae strains - comprise restriction endonuclease fragment encoding toxin, used as vaccines against cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaper JB, Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYMA-) UNIV MARYLAND BALTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9118979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cholera; vaccine; enterotoxin; diarrhoea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%;
                                                                                                                                              5667 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 5726
                                                                                                                                                                                                                                                                                                                                     5607 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 5666
                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                7 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                                                                                                                                                    GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91WO-US03812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5882..7076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "interrupted hlyA gene" complement (1193..819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "resumption of hlyA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/note= "inserted mer gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5873..1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "inserted ctxB gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.2%; Score 161; DB 13; Length 7076; 100.0%; Pred. No. 3e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; MerR; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adjacent plasmid region encoding variant MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK52213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK52213 standard; DNA; 509 BP.
The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200230962-A2.
                                                                                                                                                                                        Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000; 2000US-240465P
                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001; 2001WO-US31819
                                                                                                                                                            Disclosure; Page 25; 42pp; English.
                                                                                                                                                                                                                                                            P-PSDB; AAU97552.
                                                                                                                                                                                                                                                                                                             Summers AO,
                                                                                                                                                                                                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGCGCCTGCCATGCACGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGATGGCCGACTTGGCGCCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGGGAATGTTTCCTGCCCG 321
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                                                                                                                                                                                                                                                                                                             Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Variant MerR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC inmobilised onto a solid support, is useful for concentrating heavy metal CC ions from contaminated environment waste streams or contaminated CC elementary expressed in enteric bacteria (which are nontoxigenic and CC elementary), is suitable for use in the in vivo sequestration and CC elimination of mercuric ion from gastrointestinal tracts of animals or CC elimination of mercuric ion from gastrointestinal tracts of animals or CC elimination of the invention are also useful in water treatment resins. CC molecules of the invention are also useful in water treatment resins. CC cation such as mercury or cadmium with high affinity. The present nucleic cation such as mercury or cadmium with high affinity. The present nucleic cation for the invention are defined that encodes the variant MerR corrects of the invention are the invention of the invention of the invention are also useful in water treatment resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                ABK52206
ID ABK
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Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 509 BP; 139 A; 128 C; 140 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK52206 standard; DNA; 435 BP
                                                                                                                                                                                                               Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                               DNA encoding Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                                                        13-AUG-2002
                                                                                                                                                       Shigella flexneri.
                                                                                                                                                                                            heavy metal binding protein; MerR; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGGGAATGTTTCCTGCCCG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                         /product= "Shigella flexneri wild-type MerR protein"
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 321; DB 24; Length 509; Pred. No. 1e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
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WO200230962-A2

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cc divalent mercuric ions, to take up, sequester and concentrate the heavy cc metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when cc immobilised onto a solid support, is useful for concentrating heavy metal cons from contaminated environment waste streams or contaminated cc aqueous medium including biological fluids. The nucleic acid, when cc recombinantly expressed in enteric bacteria (which are nontoxigenic and cc recombinantly expressed in enteric bacteria (which are nontoxigenic and cc nonpathogenic), is suitable for use in the in vivo sequestration and cc elimination of mercuric ion from gastrionitestinal tracts of animals or compathogenic acid of texts metal ions such as mercury and/or cadmium. The cc molecules of the invention are also useful in water treatment resins. Cc cation such as mercury or cadmium with high affinity. The present nucleic caid sequence encodes the synthetic Merk chelon variant protein of the content of the invention. This sequence encodes one of the heavy metal binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 321 BP; 72 A; 94 C; 103 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which blinds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding the chelon protein is useful for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 21; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                   61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                                                                             CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                  Similarity
AAGGGGAATGTTTCCTGCCCG 321
                                              AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                                                     CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                           GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC
                                                                                                                                                                                                                                                                                                                                                         AGATGGCCGACTTGGCGCATGGAAAACCGTGCTGTCTGAACTCGTGTGGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 321; DB 24; Length 321; 100.0%; Pred. No. 1e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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В δÃ

1 ATGACACACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60 Matches Query Match

Local 321;

Similarity

100.0%; Score 321; DB 24; Length 354; 100.0%; Pred. No. 1e-157;

57 T; 0 other;

Conservative

0;

Mismatches

0,:

Indels

0

Gaps

60

Q В

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cc recombinant DAR molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly cc which binds mercuric ions. The invention is useful for recombinantly cc producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding the comprising a promoter active in the host cell operably linked to a coding the recombinant host cell and culturing compressed. The nucleic acid encoding the chelon protein is useful for binding complete the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding complete the neavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when combinantly expressed in enteric bacteria (which are nontoxigenic and concenting including biological fluids. The nucleic acid, when completogenic), is suitable for use in the in vivo sequestration and completogenic), is suitable for use in the in vivo sequestration and completogenic), is suitable for use in the invito sequestration and completogenic), is suitable for use in the invito sequestration and completogenic), is suitable for use in the invito sequestration and completogenic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent completogenic and enteric bacteria (which are present nucleic convention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK52212
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Sequence 354 BP; 83 A; 103 C; 111 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-435437/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYGE-) UNIV GEORGIA RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; PCR; pASK-MBD; gene; ds.
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### ALIGNMENTS

RESULT 1 ABK52207

ABK52207 standard; DNA; 321 BP

ABK52207;

13-AUG-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                               DNA encoding synthetic MerR chelon variant.
                                                                                                                                                                                                                   Synthetic.
12-OCT-2001; 2001WO-US31819
                              18-APR-2002.
                                                         WO200230962-A2
                                                                                      /product= "Synthetic MerR chelon variant"
/product= "This sequence encodes the first 107 amino acids
/note= "This sequence encodes the first 107 amino acids
of the synthetic MerR chelon variant. This
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## SUMMARIES

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                                                           AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
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/note="chelon"
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                                                                                                                                                                                                                                Direct Submission Submitted (18-DEC-2001) Kholodii G.Y., Russian Academy of Sciences, Submittee of Molecular Genetics, Kurchatov Sq. 2, Moscow 123182,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
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                                                                                                                                                                                                                 Related
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                                           /note="isolated from mercury mine, ore"
                                                                /country="Kyrgyzstan:Khaidarkan"
                                                                                                  /sex="Tra+ (narrow range)"
                                                                                                                       /db_xref="taxon:294"
                                                                                                                                         /organism="Pseudomonas fluorescens"
/strain="KHP22"
               transposon="Tn5041G"
                                                                                      /plasmid="pKHP22"
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/db_xxef="taxon:623"
/note="fn21 of Plasmid R100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-DEC-2001) Kholodii G.Y., Russian Academy of Sciences, Institute of Molecular Genetics, Kurchatov Sq. 2, Moscow 123182,
                                                                                                                                                                                                                                                                                                Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.Z. and Nikiforov,V.G. Distribution of distinct microvariants of Tn5041 in environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFL422225 445 bp DNA linear BCT 07-JUL-200. Pseudomonas fluorescens (strain KHP25) transposon Tn5041G, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                      Kholodii, G.Y.
                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                          bacteria
                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas fluorescens.
Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                            merR gene; MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence (region containing a Tn21 homologue).
                                                                                                                                                                                                                                                                                                                                                             Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                             /organism="Pseudomonas fluorescens"
/strain="KHP25"
         /country="Kyrgyzstan:Khaidarkan"
/note="isolated from mercury mine, ore"
                                              /plasmid="pKLH22"
                                                           /sex="Tra+ (narrow range)"
                                                                               /db_xref="taxon:294"
                                                                                                                                                Location/Qualifiers
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/transl_table=11
/product="Merr_p;
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of insertion of the Tn21 homologue"
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/transposon="Tn21deltaIn2"
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100.0%; r.
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Pred. No.
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119 g
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                                                                                                                                                                                                                                                                                                                                                                        merR; regulatory protein.
Alcaligenes faecalis.
Alcaligenes faecalis
                                                                                                                   Submitted (13-MAY-1994) Osborn A. M., University of Li
Genetics and Microbiology, Liverpool, Merseyside, UK,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARMERGE4 516 bp DNA linear BCT A.faecalis (SE20MERR) merR gene for regulatory protein.
                                                                                                                                                                                                                                                                               Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A. Sequence Conservation between Regulatory Mercury Resistance Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                      Z33484.1 GI:607038
                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                          from Mercury Polluted and Pristine Environments
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/protein_id="0AD19592.1"
/protein_id="0AD19592.1"
/db_xref="GI:19848213"
/translation="VETIREYQRKGLLPEPDKPYGSIRRYGEADVVRVKEVKSAQRLG
/translation="VETIRESQRKGLLPEPDKPYGSIRRYGEADVVRVKEVKSAQRLG
FSIDEIAELLRLDGGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKG
RVSCPLIASLGGEAGLARSAMP"
149 c 119 g 89 t
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/transposon="Tn21deltaIn2"
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  /clone="pSE20R1, pSE20R2" complement(13. .18)
                                                         /organism="Alcaligenes faecalis"
/isolate="SE20"
                                                                                                                                                                                                                     1 to 516)
                                           db_xref="taxon:511"
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Barrineau, P., Gilbert, P., Jackson, W.J., Jones, C.S., Summers, A.O. and Wisdom, S.
                                                                                                                                                                                                                                                                                                                                                                                                        merA gene; merR gene; merT gene; mercuric reducta
Plasmid NR1 (IncFII) from E.coli DNA, clone pDB7.
Plasmid NR1
           praft entry and sequence in computer readable form for [2] kindly provided by A.O.Summers, 15-SEP-1986. Potential Shine-Dalgarno sequences are located at positions 157-162 (13.1 kd), 590-596 (12.4 kd), 1740-1745 (59 kd) and 545-542 (15.9 kd). A single 38 bp inverted repeat, which delimits the leftward end of Tn21. Tn4 and Tn501 extends from nucleotide 65-102. A promoter region for the structural genes is located between positions 366-885. This area contains regions of dyad symmetry which might function as operator. Sites for mark, which negatively regulates the expression of the
                                                                                                                                                                                                                                                                                                The DNA sequence of the mercury resistance operon of the IncFII plasmid {\tt NR1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRIMER Plasmid NRI mercury resistance (mer) operon.
                                                                                                                                                                            Summers, A.O.
Unpublished (1986)
[2] revises [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                              K03089.1 GI:150389
structural genes as well as its own expression.
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Rygeadvyrvkfvksagrlgfsldeiaellrlddgthceeasslaehklkdvrekmad
Larmenylselvcacharkgnvscpliaslggegglarsamp"
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/protein_id="CAA83892.1"
/db_xref="GI:607039"
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/transl_table=11
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100.0%; Pred. No. 3.8e-71;
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                                                                                                                                                                                                                                                /protein_id="aab59077.1"
/db_xref="G1:150395"
/translation="McLAWTRIADKTGALGSVVSAMGCAACFPALASFGAAIGLGFLSQ
YEGLFISRLLPLFAALAFLANALGWESHRQWLESLLGWIGPAIVFAATVWLLGNWWTA
NLMYVGLALMIGVSIWDFVSPAHRRCGPDGCELPAKRL"
                          /translation="MSTLKITGMTCDSCAVHVKDALEKVPGVQSADVSYAKGSAKLAIEVGTSPDALTAAVAGLGYRATLADAASVSTPGGLLDKMRDLLGRNDKTGSSGALHIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_io="ABB9076.1"
/db_xref="GI:150394"
/translation="MKKLFASLALAAAVAPVWAATQTVTLAVPGMTCAACPITVKKAL
KVEGVTKVDVGFEKREAVVTFDDTKASVQKLTKATADAGYPSSVKQ"
                                                                                   /transl_table=11
/protein_id="AAB59078.1"
/db_xref="GI:150396"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSEPQNGRGALFAGGLAAILASTCCLGPLVLVALGFSGAWIGNLTVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLVLVALGFPYVVPFFY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/protein_id="AAB59074.1"
/db_xref="GI:150392"
/translation="MRAKSAIFSRTSLSLCSARLLASSQWVPSSSRNSSAISSRLNPS
IGSGGAAMAAALKAVEQGARVTLIERGTIGGTCVNVGCVPSKIMIRAAHIAHLRRESP
                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                    'note="Hg(II) reductase (59.0 kd merA)"
                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="15.0 kd merTC protein"
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/db_xref="GI:150391"
/translation="MAGAHEERQHGFHARQVGHLLAHVLELVFGQAAGLLAVGATVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="G1:455296"
/translation="mennlenltigyfakaagvnvetirfygrkgllrepdkpygsir
/translation="mennlenltigyfakaagvnvetirfygrkgllrepdkpygsir
/translation="mennlengtherepdkpygsir
/tryselvcacharkgnvscpliaslggeaglarsamp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="9.4 kd merTB protein"
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/db_xref="GI:150393"
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/note="15.9 kd merR protein"
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                           Misra,T.K., Brown,N.L., Fritzinger,D.C., Pridmore,R.D., Barnes,W.M., Haberstroh,L. and Silver,S.
Mercuric inor-resistance operons of plasmid R100 and transposon Tn501: the beginning of the operon including the regulatory region and the first two structural genes
Proc. Natl. Acad. Sci. U.S.A. 81 (19), 5975-5979 (1984)
                                                                                                                                                                6265806
                                                                                                                                                                                                                               Ohtsubo,H., Nyman,K., Doroszkiewicz,W. and Ohtsubo,E. Multiple copies of iso-insertion sequences of IS1 in Shigella dysenteriae chromosome
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IYQLANDGGERVVAFDRCLIAPGASPAVPPIPGLKDTPYWTSTEALVSETIPKRLAVIG
SSVVALELAQAFARLGAKVTILARSTLFFREDPAIGEAVTAAFRAEGIEVREHTQASQ
VAXINGEGDGEFVLTTPAHGELRADKLLVATGRAPNTBKLADATGVTLTPGGAIVIIDP
GMRTSVEHIYAAGDCTDQPQFVYVAAAAGTRAAINMTGGDAALNLTAMPAVVFTDPQV
ATVGTSEAEÄHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cause loss of translocation activity.

Three R100 derived small circular plasmids (pSM1, pSM2, pSM5) from the R100 derived small circular plasmids (pSM1, pSM2, pSM5) from the same as pSM2, except for a ISIR) in circularized form. pSM1 is the same as pSM2, except for a psychological part of the same as pSM2, except for a perfect of the same psychological properties and psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psychological psycholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence for [3], [5] and [4] kindly provided on tape by T.K.Misra. Isl from [1] was renamed ISlR after [2] discovered that there are several ISl iso-insertion sequences. The 5' and 3' ends of ISlR are approximate inverted repeats. [2] found the CDS regions annotated below conserved among several ISls. Deletion mutations in either of these two coding frames or in the two ends of ISlR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Silver, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (bases 4348 to 5747)
Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A., Lien, C., Sieff, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mercuric reductase structural genes from plasmid R100 and transposon Tn501: functional domains of the enzyme Gene 34 (2-3), 253-262 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silver, S.
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Potential -35 regions are found at positions 980-984 and 1402-1406 and -10 regions at positions 999-1006 and 1425-1431. Unidentified reading frames are found at positions 2143-2565, 4688-4924 (gtg start codon), and 4921 to 5593. [4] noted two other ORF's in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vicinity of the merR gene. [2] sites; insA and insB spans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2989109
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103. .870
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929. .966
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1080. .1262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative"
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                                                                                                                              'note="Tn21 inverted repeat"
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Best Local :
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                                                                             67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                           7 CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                  Similarity
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4329. .4691
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2617. .4311
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1832. .2107
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'gene="merT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {	t ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA}
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/gene="merA"
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                                                                                                                                                                                                                                                                         Score 161; DB 1; Length 5747; Pred. No. 2.7e-71;
                                                                                                                                                                                                                                             0; Mismatches
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85283620 85283620 2992807 7 (bases 14935 to 15434) 8rown,N.L., Misra,T.K., Winnie,J.N., Schmidt,A., Seiff,M. and Silver,S. The nucleotide sequence of the mercuric resistance operons of plasmid R100 and transposon Tn501: further evidence for mer genes which enhance the activity of the mercuric ion detoxification	8), 2135-2141 (198 057 to 4105) nd Tu,C.P. el regulatory gene cointegrate resolu	MISTA,T.K., Brown,N.L., Haberstroh,L., Schmidt,A., Goddette,D. and Silver,S.  Mercuric reductase structural genes from plasmid R100 and transposon Tn501: functional domains of the enzyme Gene 34 (2-3), 253-262 (1985)  85232071 2989109 5 (bases 2952 to 4066) Rogowsky,P., Halford,S.E. and Schmitt,R. Definition of three resolvase binding sites at the res loci of Tn21	and Wisdom, S. and Wisdom, S. The DNA sequence of the mercury resistance operon of the IncFII plasmid NR1 J. Mol. Appl. Genet. 2 (6), 601-619 (1984) 85159407 6530603 4 (bases 16253 to 18549)	perons of plasm he operon inclural genes S.A. 81 (19), 5	Altenbuchner J., Rogowsky, P. and Schmitt, R.  Altenbuchner J., Rogowsky, P. and Schmitt, R.  DNA sequences of and complementation by the tnpR genes of Tn21,  Tn501 and Tn1721  Mol. Gen. Genet. 191 (2), 189-193 (1983)  84013495  6312271  2 (bases 18411 to 19672)  Misra. T. K. Brown N. I. Fritzinger D. G. Bridger D. G.  Misra. T. K. Brown N. I. Fritzinger D. G. Bridger D. G.  Misra. T. K. Brown N. I. Fritzinger D. G. Bridger D. G.  Misra. T. K. Brown N. I. Fritzinger D. G. Bridger D. G.  Misra. T. K. Brown N. I. Fritzinger D. G. Bridger D. G.  Misra. T. K. Brown N. I. Fritzinger D. G. Bridger D. G. Brider D. G. Bridger D. G. Bridger D. G. Bridger D. G. Bridger D. G.	AF071413 Asembled sequence of transposon In2l cont genes, the integron In2, and the mercury r AF071413 AF071413 AF071413.2 GI:21930298 Escherichia coli Escherichia coli Escherichia; Proteobacteria; gamma subdivisio Escherichia 1 (Dases 2952 to 4066)	
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antibiotic-resistance genes of several integrons  Gene 142 (1), 49-54 (1994)  94237488  8181756 17 (bases 4492 to 8992) Recchia.G.D., Stokes,H.W. and Hall,R.M. Characterisation of specific and secondary recombination sites recognised by the integron DNA integrase Nucleic Acids Res. 22 (11), 2071-2078 (1994)	metal-responsive transcription (1992) 7-3101 (1992) and Roy, P.H. archem promoters for	2163386 14 (bases 14967 to 15674) 14 (bases 14967 to 15674) 14 (bases 14967 to 15674) 15 (bases 111 (1), 11-20 (1992) 15 (bases 19146 to 19199) 15 (bases 19146 to 19199)	2190244  13 (bases 4106 to 5438)  13 (bases 4106 to 5438)  Mercier,J., Lachapelle,J., Couture,F., Lafond,M., Vezina,G.,  Boissinot,M. and Levesque,R.C.  Structural and functional characterization of tnpI, a recombinase locus in Tn21 and related beta-lactamase transposons  J. Bacteriol. 172 (7), 3745-3757 (1990)	site-specific gene-integration functions: integrons Mol. Microbiol. 3 (12), 1669-1683 (1989) 90158115 2560119 12 (bases 6301 to 6333) Guerineau,F., Brooks,L. and Mullineaux,P. Expression of the sulfonamide resistance gene from plasmid R46 Plasmid 23 (1), 35-41 (1990) 90272799	site-directed specific recombination and gene expression in Tn21 transposons  L Mol. Microbiol. 3 (11), 1545-1555 (1989)  E 90136084  DD 2559298  T1 (bases 7540 to 9257)  S Stokes, H.W. and Hall, R.M.  A novel family of potentially mobile DNA elements encoding	veen toterizer	system Mol. Gen. Genet. 202 (1), 143-151 (1986) 86174347 3007931 8 (bases 1 to 3056) Ward, E. and Grinsted, J. The nucleotide sequence of the tnpA gene of Tn21 Nucleic Acids Res. 15 (4), 1799-1806 (1987) 87146495

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Gene cassettes: a new class of mobile element
Microbiology 141 (Pt 12), 3015-3027 (1995)
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Brown, H.J., Stokes, H.W. and Hall, R.M.
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Partridge,S.R. and Hall,R.M.
In34, a complex In5-like class 1 integron containing orf513 and
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EIGRPRSERKLPVVLTPDEVVRILGETLEGEHELFAQLLYGTGMRISEGLQLRVKDLDF
EIGRPRSERKLPVVLTPDEVVRILGETLEGEHELFAQLLYGTGMRISEGLQLRVKDLDF
EIGRFRSERKLPVVLTPDEVVRILGETLEGELSRARWMLKDQAEGRSGVALLPDALER
KYPRAGHSWPWFWVFAQHHHSTDPRSGVVRRHHMYDOTFQRAFKRAVEQAGITKPATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="may confer resistance to erythromycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mphA"
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/gene="sull"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="sull"
7600. .8439
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/protein_id-"AAG14403.1"
/protein_id-"AAG14403.1"
/db_xref-"G1:10185691"
/translation-"MTGQRIGYIRVSTFDQNPERQLEGVKVDRAFSDKASGKDVKRPQ
/translation-"MTGQRIGYIRVSTFDQNPERQLEGVKVDRAFSDKASGKDVKRPQ
LEALISFARTGDTVVVHSMDRLARNILDDLRRIVQTLTQRGVHIEFVKEHLSFTGEDSP
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Submitted (18-MAY 1999) Gen-ichi Sampei, The University Electro-Communications, Department of Applied Physics an Chemistry; 1-5-1, Chofugaoka, Chofu, Tokyo 182-8585, Jap (E-mail:sampei@pc.uec.ac.jp, Tel:81-424-43-5492,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  merR; merT; merC; merA; merD; yadA; yaeA; tniA; tniBdeltal; yahA; istB; ybbA; sult; qaceEdeltal; addAl; intR; tnpM; tnpR; tnpA; ybjA; cat; insA; insB; ycdA; ycdB; stbB; stbA; ycgA; ycgB; ychA; yciA; yciB; ycjA; ycjB; ydaA; ydbA; ydcA; yddA; ycgB; ychA; ydjA; ydjA; ydjB; yeaA; tetR; tetA; tetC; tetD; yedA; yefA; yafB; psiA; mok; hok; yehA; yeiA; 32; X; traM; finP; traJ; traY; traB; traE; traK; traB; traD; traY; traR; yfhA; yfiB; yfiC; traC; trbI; traW; traU; ygeA; trbC; traN; traZ; trbB; traB; traU; ygeA; trbC; traN; traZ; yhfA; traD; traI; traX; yieA; finO; yigA; yigB; yihA; repA2; inC; plasmid R100 (specific_host:Shigella flexneri 2b strain 222, ash boot-repActaria; craci; traC; t
                                                                                                                                                                                                                                   Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                         Organization and diversification of plasmid
                                                                                                                                                  Sampei, G. and Mizobuchi, K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                   Sampei, G. and Mizobuchi, K.
                                                                                                                                                                                                                                                                                nucleotide sequence of the R100 genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid R100 DNA, complete sequence.
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7506 c 7633 q
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/protein_id="AAG14408.1"
/db_xref="GI:10185696"
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/note="Plasmid R100 is also referred to as NR1 or R222"
join(59. .7369,11456. .19730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(92. .526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(92. .526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /specific_host="Shigella flexneri 2b strain 222"
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Rygeadvyrvkfyksagrigfsidelaeilriddgthceeassiaehkikdvrekmad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="msepQngrgalfagglaailasTccLgpLvLvaLgfSgAwignL
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/db_xref="GI:5103149"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="100% identical to gp:NRIMER_I[Merr of plasmid NRI]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Plasmid R100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="100% identical to gp:NRIMER_4[MerT of plasmid NR1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LARMETVLSELVCACHARKGNVSCPLIASLQGEAGLARSAMP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transposon="Tn21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVALGFPYVVPFFY"
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1234. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="100% identical to gp:NRIMER_5[MerP of plasmid NR1]"
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                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                       transl_table=11
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                                                                     codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .94281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          merp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                merT"
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/Translation="MSTLKITGMICDSCAVHVKDALEKVPGVQSADVSYAKGSAKLAI
/Translation="MSTLKITGMICDSCAVHVKDALEKVPGVQSADVSYAKGSAKLAI
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QAYINGEGDGEFVLTTAHGELRADKLLVATGRAPNTRLALDATGVTLTPQGAIVIDP
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GMRTSVEHIYAAGDCTDQPQTYVAAAAGTRAAINMTGGDAALNLTAMPAVVFTDPQV
ATVGSSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLLGVQAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSAYTVSQLAHNAGVSVHIVRDYLVRGLLRDVACTTGGYGVFDD AALQRLCFVRAAFEAGIGLDALARLCRALDAADGAQAAAQLAVLRQLVERRRAALAHL DAQLASMPAERAHEEALP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3459
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/gene="merD"
                                                                                                                                                                                                                                                                                                                                                                                                                                              4833. .6512
/gene="tniA"
4833. .6512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAGELIQTAALAIRNRMTVQELADQLFPYLTMVEGLKLAAQTFNKDVKQLSCCAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="GI:5103153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAFLGEHWGVAALALTGLFVLAVTRLLRAFRGGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function unknown]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRWRHPRLGLLPPGOFLPLAESFGLMPEIGAMVLGEACROMHKWOGPAWOPFRLAINV
SASQVGPTFDDEVKRYLADMALPAELLEIELTESVAFGNPALFASFDALRAIGVRFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene product of plasmid
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                                                                                                                       /translation="MATDTPRIPEQGYATLPDEAWERARRRAEIISPLAQSETYGHEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDFGTGYSCLOHLKCCPITTLKIDQSFVARLPDDARDQTIVRAVIQLAHGLGMDVIFR
RRLHQLIGRNGCCAASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA78791.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(4692. .7369,11456. .15691)
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="yaeA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="100% identical to gp:ECOMERTET_3[urf1, putative
RF, gene product of plasmid R100]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="yadA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="yadA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transposon="In2"
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                             LRRGCEQHGIRLDYRPLGQPHYGGIVERIIGTAMQMIHDELPGTTFSNPDQRGDYDSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gp:ECOMERTET_4[urf2, putative ORF,
R100]"
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CDS

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cps

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COMMENT
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                                                                                                         TITLE
                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                          TITLE
                                                                              JOURNAL
                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286
Direct Submission
Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                      Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Fettwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T. S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (8658), 848-852 (2001)
                                                                                                                Parkhill, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enterica subsp. enterica serovar Typhi. Salmonella enterica subsp. enterica serovar Typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL513383.1 GI:16505740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid pHCM1
AL513383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STYPPHCM1
                                                                                                                                                                   1677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 218160)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 218160)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /insertion_seq="IS1326"
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NSVNRREFLNLLRFLGNELRIPLVGVGTRDAYLAIRSDDQLENRFEPMMLPVWEANDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALNRLEALYAWPNKQRMPNLLLVGPTNNGKSMIVEKFRRTHPASSDADQEHIPVLVVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCSLLASFAASLPLRRPSPIATLDMARYLLTRSEGTIGELAHLLMAAAIVAVESGEEA
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GQHYLLIPYBTLSHPAVTLWEQRQALAKLRQQGREQVDESALFRWIGQMREIYTSAQK
ATRKARRDADRRQHLKTSARPDKPVPPDTDIADPQADNLPPAKPFDQIEEW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INHRTLSMAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="100% identical to gp:TTU42226_7 [TniBdeltal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="tniBdeltal"
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100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.2%; Score 161; DB 1; 100.0%; Pred. No. 1.8e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tniBdeltal"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.
/note="HCM1.04c, insB, possible IS1 transposase, len: 156 aa; highly similar to many from Enterobacteriaceae e.g. SW:ISB_ECOLI (EMBL:D10483), insB, Escherichia coli insertion element IS1 protein InsB (167 aa), fasta scores; E(): 0, 91.6% identity in 167 aa overlap"
                                                                                                                                        complement(1876. .2346)
/gene="insB"
                                                                                                                                                                                                              complement(1876, .2346)
/gene="insB"
                                                                                                                                                                                                                                                                                                           complement(1871. .2585)
/note="IS1"
                                                                                                                                                                                                                                                /note="13 bp inverted repeat flanking IS1"
                                                                                                                                                                                                                                                                                                                                                       /note="possible RBS"
                                                                                                                                                                                                                                                                                                                                                                                                                   /product-hypothetical protein protein /protein_id-"CAD09621.1"
/protein_id-"CAD09621.1"
/db_xref-"61:16505743"
/translation-"MNKPLVSFAELSGNAINVARQSVIDMEMDATREKIGKARSLFHS
/TITANSLATION-"MNKPLVSFAELSGNAINVARQSVIDMEMDATREKIGKARSLFHS
GIHRAVNGYPLIQSAANQLAVIKRLLGDTKYLDACITENLCMFSPEGYLYLFMQRRFI
                                                                                                                                                                                    /note="HCM1.04c"
                                                                                                                                                                                                                                                                                                                                                                                 complement(1697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="HCM1.03c, hypothetical protein, len: 107 aa;
unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1367. .1690)
/gene="HCM1.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HCM1.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="hypothetical protein"
/protein_id="CAD09620.1"
/db_xref="GI:16505742"
/translation="MMYPDITGVKMKLSQLEVGMTVWSLSRTKMGNTTIKTVTLHSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(742. .1053)
/gene="HCM1.02c"
complement(742. .1053)
/gene="HCM1.02c"
/note="HCM1.02c"
/note="HCM1.02c, hypothetical protein, len: 103 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(536. .540)
/note="possible RBS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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RRLTYTRLDEELEKIA"
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katfevnggllmalllallmlvciiqrlatgdrlmsftgepdvrdiqftlmlviefal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative membrane protein"
/protein_id="CAD09619.1"
/db_xref="GI:16505741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane-spanning regions. Spans sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1, .528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HCM1.01c"
complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEVHDNHVIASWNGNAPRRFGETAITGWKKEKPLLIRDRSGSARLATREEKARILDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="HCM1.01c, possible membrane protein, len: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Salmonella enterica subsp. enterica
Typhi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /plasmid-"pHCM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ps00017 ATP/GTP-binding site motif A (P-loop)"
complement(2573, .2585)
/note="13 bp inverted repeat flanking IS1"
complement(2694, .3644)
/gene="corA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative IS1 transposase"
/protein_id="0AD09623.1"
/db_xref="G1:16505745"
/translation="MASVSISCPSCSATDGVVRNGKSTAGHQRYLCSHCRKTWQLQFT
/TASDPCTHQKIIDMAMNGYGCRATARIMGVGLNTILRHLKNSGRSR*
YTASQPCTHQKIIDMAMNGYGCRATARIMGVGLNTILRHLKNSGRSR*
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/db_xref="g1:16505744"
/translation="Mpgnrphygrwpohdetsfkklrpogvtsriopgsdvivcaksr
/translation="Mpgnrphygremmatigrimsilspedvvimmtdgwplyesrikgk
ormieyandrierhnlniendhlarigrkslsfsksvelhdkvighvlnikhvq"
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/protein_id="CAD09622.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="HCM1.07c, corA, probable magnesium and cobalt transport protein, len: 316 aa; similar to many e.g. SW:CORA_ECOLI (EMBL:L11042), corA, Escherichia coli magnesium and cobalt transport protein (316 aa), fasta scores; E(): 0, 99.1% identity in 316 aa overlap. Contains perm match to entry PF01544 CorA, CorA-like Mg2+transporter protein. Contains hydrophobic, possible membrane-spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"possible translational frameshift site, similar to that determined experimentally (EMBL:X52534)" complement(2472. .2495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2265. .2540)
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/gene="corA"
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                                                                                                                                                                                                                                                                                                                                                                           GMNFEFMPELKWRFGYPAAIIFMILAGLAPYLYFKRKNWL" complement(2697. .3584)
                                                                                                                                                                                                                                                                                                                                                                                                                                 ELGQSLATRPELEDIEASARFFEDDOCHHIHSFFFFEDAEDHAGNSTVAFTIRDGRLF
TLRERELPAFRLYRMARSQSMVDGNAYELLLDLFETKIEQLADEIENIYSDLEQLSR
VIMEGHQGDEYDEALSTLAELEDIGWKVRLCLMDTQRALNFLYRKARLDGGQLEQARE
ILRDIESLLPHNESLFQKVNFLMQAAMGFINIEQNRIIKIFSVVSVVFLPPTLVASSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative magnesium and cobalt transport protein" /protein_id="CAD09624.1" /db_xref="GI:16505746" /db_xref="GI:16505746" /translation="MLSAFQLENNRLTRLEVEESQPLVNAVWIDLVEPDDDERLRLQS
                                                                                                                                                                                                                                                    transporter protein, sc
complement(3653...3656)
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/gene="HCM1.08"
/note="HCM1.08, hypothetical protein, len: 109 aa;
                                                                                         /gene="HCM1.08"
                                                                                                                                                                                                                                                                                                              note="Pfam match to entry
                                                                                                                          -"possible RBS"
.4343
                                                                                                                                                                                                                    possible RBS"
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score 432.90, E-value 2.8e-126"
                      similar
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DEFINITION
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                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                      TITLE
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             -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.oxytoca (SE31MERR) merR gene for regulatory protein
                                                                                                                                                                                                                                                                                        Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A. Sequence Conservation between Regulatory Mercury Resistance Genes from Mercury Polluted and Pristine Environments
                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella oxytoca.
Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                            merR gene; regulatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFMERGE5
                                                                                                                                                                                Submitted (13-MAY-1994) Osborn A. M., University of Genetics and Microbiology, Liverpool, Merseyside,
                                                                                                                                                                                                                     Osborn, A.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                    Klebsiella
                                                                                                                                                                                                                                                     (bases 1 to 537)
                                                                                                                                                                                                                                                                                                                                             (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the N-terminal half of SW:YIGE_ECOLI (EMBL:L02122), yigE, Escherichia coli hypothetical protein (254 aa), fasta scores; E(): 0, 97.9% identity in 95 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4363. .4569)
/gene="HCM1.10c"
/note="HCM1.10c, hypothetical protein, len: 68 aa; unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4363. .4569)
/gene="HCM1.10c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQAYTVNPQTERVKMYWQKANGEAWGTLHALLADINSQGQVQMAMNGGILNLTVFDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="CAD09625.1"
/db_xref="GI:16505747"
/translation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"hypothetical protein"
/protein_id="CAD09626.1"
/db_xref="GI:16505748"
/translation="MGHYDYTRTLRYQLYDASRFHDGATAEQAGELHTVAFSKPAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRKKEVF'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11
                                                      /clone="psE31R1, psE31R2, complement(13. .18)
                 complement(28.
                                                                                                                           /organism="Klebsiella oxytoca"
                                    /citation=[1]
                                                                                         /db_xref="taxon:571"
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/citation=[1]
                                                                                                          'isolate="SE31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.2%; Score 161; DB 1; 100.0%; Pred. No. 1.6e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                     . 33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 bp
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                                                                             pSE31R3"
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ECU77087/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-NOV-1996) Microbiology, University of Georgia, 527 Biological Sciences, Athens, GA 30602-2605, USA
                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia.

1 (bases 1 to 1696)

Ogawa, H. I., Tolle, C. L. and Summers, A. O.

Physical and genetic map of the organomercury resistance (Omr) and inorganic mercury resistance (Hgr) loci of the IncM plasmid R831b gene 32 (3), 311-320 (1984)
                                                                                                                                                                                                                                                                                                        Liebert, C.A., Watson, A.L. and Summers, A.O.
                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the organomercury resistance (OMR) locus Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                      Tolle, C., Totis, P. and Summers, A.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
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Escherichia coli
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mercury resistance; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U77087.1 GI:1679729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli plasmid R831b organomercury resistance (OMR) locus: mer operon regulatory protein (merR) and organomercurial lyase (merB) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%; Conservative 0;
                                                                            complement(1. .305)
/note="similar to GenBank Accession Numbers M24940 and
00777; partial 5' tnpA gene and tnpA promoter region"
complement(36. .740)
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/db_xref="taxon:562"
/plasmid="R831b"
                                              complement(306. .740)
/note="similar to GenBank Accession Number M24940; mer
                                                                    /gene="merR"
                                                                                                                                                                                                                                     Location/Qualifiers
                              /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:Q57492"
/translation="MQINFERLTIGVEAKAAGVNVETIREYQRKGLLPEPDKPYGSIR
RYGEADVTRYFYKSAQRLGFSLDEIAELLRLEDGTHCEEASGLAEHKLKDVREKMAD
LARMEAVLSELVCACHARKGRVSCPLLASLQDGTKLAASARGSHGVTMP"
136 c 175 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="regulatory protein"
/protein_id="CAA83893.1"
/db_xref="GI:607037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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72. .527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /citation=[1]
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                                                                                                                                                                                                                       .1696
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Job time : 1800 secs
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                                                                                                                        175 GGCACCCACTGCGAGGAGGCCAGCAGCCTGGCCGA 209
                                                                               506 GGCACCCACTGCGAGGAGGCCAGCAGCCTGGCCGA 472
                                                                                                                                                                              35,
                                                                                                                                                                         Conservative
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ILDWPAERVAAVLEQATSTEYDKDGNIIGYGLTLRETSYVFEIDDRRLYAWCALDTLI
FPALIGRTARVSSHCAATGAFVSLTVSPSEIQAVEPAGMAVSLVLPQEAADVRQSFCC
HVHFFASVPTAEDWASKHQGLEGLAIVSVHEAFGLGQEFNRHLLQTMSSRTP"
487 c 460 g 367 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similiar to merA sequence, GenBank Accession
Numbers M15049 and KO3089; truncated 3' nonfunctional end
of merA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="possible merB -10 signal site"
complement(773, .778)
/note="possible merR -10 signal site"
complement(793, .798)
                                                                                                                                                                                                                                                                                                                                                                                             /product="MerB"
/protein_id="AAB49639.1"
/db_xref="GI:1679731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organomercurial lyase"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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LARMEAVLSDLVCACHSROGNVSCPLIASLQGGTSLAGASTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GenBank Accession Number M15049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="merB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(793. .798)
/note="possible merR -35 signal site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="merB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="18 base pair hyphenated dyad; MerR binding site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           operon regulatory protein*
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="possible merB -35 signal site"
                                                                                                                                                                                     10.9%; Score 35;
100.0%; Pred. No.
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